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SPDI search SEQ ID NO:38 commercial and interference.

Thanks.

AA 720

Patricia A. Duffy, Ph.D.

Primary Patent Examiner

571-272-0855,

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OM protein - protein search, using sw model

Run on: April 4, 2007, 21:57:24 ; Search time 347 Seconds

(without alignments)
2224.581 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945

Sequence: 1 MELGCVTQGLTFLLQLLLS.....LSTAPTKVLPEKDWIERNNK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 1500 summaries

Database :

1: uniprot_8.4.*

2: uniprot_sprot.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3945	100.0	720	2	Q6UXH9_HUMAN
2	3941	99.9	720	2	Q5JPI4_HUMAN
3	3936	99.8	720	2	Q6N062_HUMAN
4	3926.5	99.5	737	2	Q5EBU7_HUMAN
5	3921.5	99.4	737	2	Q96UW2_HUMAN
6	3898	98.8	720	2	Q5RDI1_PONPY
7	3616	91.7	720	2	Q5E9P5_BOVIN
8	3612	91.6	720	2	Q8BU25_MOUSE
9	3612	91.6	720	2	Q8K2B8_MOUSE
10	2823	71.6	722	2	Q6DIV5_XENTR
11	2059	52.2	417	2	Q71RE9_HUMAN
12	1566	39.7	1009	2	Q4SAF4_TETNG
13	1122.5	28.5	488	2	Q4SHD4_TETNG
14	949	24.1	181	2	Q9Y432_HUMAN
15	678	17.2	1019	2	Q8Y321_TACTR
16	672	16.9	1019	1	LFC_TACTR
17	665	16.9	1019	1	LFC_CARRO
18	665	15.4	1083	2	Q26423_CARRO
19	608.5	15.4	680	2	Q868H7_BRABE
20	604	15.3	680	2	Q868H5_BRABE
21	597	15.1	688	2	Q868H6_BRABE
22	576.5	14.6	688	2	Q868H4_BRABE
23	507.5	12.9	730	2	Q6GPF9_XENLA
24	490.5	12.4	698	2	Q6Q1Q8_CHICK
25	489.5	12.4	698	2	Q9PU11_XENLA
26	483	12.2	701	2	Q9JUS9_RAT
27	482.5	12.2	703	2	Q8CHN6_RAT
28	482	12.2	717	2	Q8AXR1_XENLA
29	478	12.1	699	1	MASPI_HUMAN
30	475	12.0	704	1	MASPI_MOUSE
31	468	11.9	728	2	Q96RS4_HUMAN

32	467	11.8	697	2	Q8CG43_RAT	Q8CG43_rattus norv
33	466	11.8	717	2	Q8AXR0_XENLA	Q8AXR0_xenopus lae
34	459	11.6	733	2	Q8CD27_MOUSE	Q8CD27_mus musc
35	457	11.6	719	2	Q9PYV2_TRISC	Q9PYV2_titiaki scy
36	452	11.5	733	2	Q920S0_MOUSE	Q920S0_mus muscu
37	450.5	11.4	687	2	Q5XHB9_XENTR	Q5XHB9_xenopus tro
38	448	11.4	745	2	Q9PYV3_CYPCA	Q9PYV3_cyprinus ca
39	447	11.4	686	2	Q6Q1Q9_CHICK	Q6Q1Q9_gallus gall
40	436.5	11.1	681	2	Q7ZT70_LAMJA	Q7ZT70_lampectra ja
41	432.5	11.0	745	2	Q4SB49_TETNG	Q4SB49_tetraodon n
42	428	10.8	707	1	C1RA_MOUSE	Q8CG16_mus muscu
43	428	10.8	707	1	Q56616_MOUSE	Q56616_mus muscu
44	423	10.7	685	1	MASP2_RAT	Q9J188_r_mannan-bi
45	422.5	10.7	713	2	Q5DVT1_EPRBU	Q5DVT1_epitretus
46	421.5	10.7	688	2	Q9PYV4_XENLA	Q9PYV4_xenopus lae
47	417	10.6	685	1	MASP2_MOUSE	Q91WPO_m_mannan-bi
48	416.5	10.6	706	1	C1RB_MOUSE	Q8CF99_mus muscu
49	414	10.5	708	2	Q2VFN1_XENLA	Q2VFN1_xenopus lae
50	404.5	10.3	705	2	Q5HTF9_HUMAN	Q5HTF9_homo sapien
51	403.5	10.2	705	1	C1R_HUMAN	P00736_homo sapien
52	403.5	10.2	705	2	Q6BD77_HUMAN	Q6BD77_homo sapien
53	401.5	10.2	496	2	Q8CHP7_CAVPO	Q8CHP7_cavia porce
54	401.5	10.2	746	2	Q81AD8_HAIRO	Q81AD8_haloecynthia
55	400.5	10.2	686	1	MASP2_HUMAN	Q00187_h_mannan-bi
56	400.5	10.2	746	2	Q01654_HAIRO	Q01654_haloecynthia
57	398.5	10.1	686	2	Q9DGC2_CYPCA	Q9DGC2_cyprinus ca
58	395.5	10.0	705	2	Q53HU9_HUMAN	Q53HU9_homo sapien
59	395	10.0	721	2	Q7ZT69_LAMJA	Q7ZT69_lampectra ja
60	394.5	10.0	705	1	C1R_PANTR	Q51W33_pan troglod
61	394.5	10.0	705	1	C1R_PONPY	Q51544_pongo pygma
62	390.5	9.9	702	2	Q4SNE6_TETNG	Q4SNE6_tetraodon n
63	390.5	9.9	705	2	Q4R577_MACPA	Q4R577_macaca fasc
64	384	9.7	688	1	CS1B_MOUSE	Q8CF98_mus muscu
65	382.5	9.7	752	2	Q01655_HAIRO	Q01655_haloecynthia
66	382	9.7	722	2	Q8AW90_LAMJA	Q8AW90_lampectra ja
67	381	9.7	722	2	Q9PEZ5_LAMJA	Q9PEZ5_lampectra ja
68	380.5	9.6	687	1	C1S_PIG	Q694D8_sus scrofa
69	378.5	9.6	695	1	CABE_MESAU	P15156_mesocricetu
70	378	9.6	676	2	Q4SBS1_TETNG	Q4SBS1_tetraodon n
71	373.5	9.5	688	2	Q4SNE7_TETNG	Q4SNE7_tetraodon n
72	372.5	9.4	752	2	Q81AD7_HAIRO	Q81AD7_haloecynthia
73	368	9.3	685	2	Q9DGC1_CYPCA	Q9DGC1_cyprinus ca
74	366	9.3	685	2	Q9DGC0_CYPCA	Q9DGC0_cyprinus ca
75	364	9.2	688	1	CS1A_MOUSE	Q8CG14_mus muscu
76	359	9.1	685	2	Q3V5Q0_CYPCA	Q3V5Q0_cyprinus ca
77	357	9.0	676	2	Q6DUJ6_CYPCA	Q6DUJ6_cyprinus ca
78	354	9.0	1524	2	Q91674_XENLA	Q91674_xenopus lae
79	346	8.8	690	2	Q5F3N3_CHICK	Q5F3N3_gallus gall
80	345	8.7	638	2	Q17H79_ABDAA	Q17H79_aedes aegyp
81	340.5	8.6	688	1	C1S_RAT	Q6P6T1_rattus norv
82	340	8.6	688	2	Q3T9K7_MOUSE	Q3T9K7_mus muscu
83	339.5	8.6	707	2	Q70W31_ONCYH	Q70W31_oncorhynch
84	337.5	8.6	479	2	Q5HYM1_HUMAN	Q5HYM1_homo sapien
85	337.5	8.6	608	2	Q7PY92_ANOGA	Q7PY92_anopheles g
86	335	8.5	666	2	Q69BL0_MANSE	Q69BL0_manduca sex
87	334	8.5	503	2	Q8AYE4_BRABE	Q8AYE4_brachydanio
88	334	8.5	688	1	C1S_HUMAN	P09871_homo sapien
89	333	8.4	730	2	Q4RHT0_TETNG	Q4RHT0_tetraodon n
90	331.5	8.4	1019	2	Q4RHT0_TETNG	P98070_homo sapien
91	331.5	8.4	1019	2	Q2NKL7_HUMAN	P29K17_homo sapien
92	330.5	8.4	1034	1	ENTK_PIG	P98074_sus scrofa
93	329.5	8.4	3565	1	CSMD1_HUMAN	Q96P27_homo sapien
94	329	8.3	3564	1	CSMD1_MOUSE	Q92313_mus muscu
95	328.5	8.3	2966	2	Q59FF8_HUMAN	Q59FF8_homo sapien
96	328	8.3	855	1	ST14_HUMAN	Q9Y5V6_h suppresso
97	325	8.2	483	1	FA10_TROCA	Q4GT95_tropidichis
98	324	8.2	3564	2	Q4SNC2_RAT	Q4SNC2_rattus norv
99	319.5	8.1	455	1	FA10V_TROCA	P81428_tropidichis
100	319.5	8.1	455	2	Q11657_TROCA	Q11657_tropidichis
101	318.5	8.1	455	2	Q4F879_9SAUR	Q4F879_notechis sc
102	318	8.1	483	2	Q11659_PSETE	Q11659_pseudonaja
103	318	8.1	827	2	Q1RLP8_BRABE	Q1RLP8_brachydanio
104	318	8.1	3487	1	CSMD2_HUMAN	Q72408_homo sapien

105	318	8.1	3631	2	Q53TV4_HUMAN	Q53TV4_homo sapien	178	281.5	7.1	476	2	Q6GLK4_XENLA	Q6GLK4_xenopus lae
106	317.5	8.0	455	2	Q58L92_HOPEST	Q58L92_hoplostethal	179	281.5	7.1	558	1	HABP2_MOUSE	Q8K0D2_m_hyaluron
107	317.5	8.0	1035	1	ENTK_BOVIN	P98072_bos taurus	180	281.5	7.1	558	1	HABP2_RAT	Q61111_r_hyaluron
108	316.5	8.0	460	1	PROC_MOUSE	P33587_m vitamin k	181	281	7.1	481	1	FA10_MOUSE	Q88947_mus musc
109	315	8.0	444	1	FA7_RABIT	P98139_oryctolagus	182	281	7.1	481	2	Q4F0S7_MOUSE	Q4F0S7_mus musc
110	314.5	8.0	454	2	Q58L93_PSEPO	Q58L93_pseudochis	183	281	7.1	481	2	Q3TRR2_MOUSE	Q3TRR2_m nod-deriv
111	314.5	8.0	475	1	FA10_CHICK	P56157_gallus gall	184	281	7.1	483	2	Q3MHW2_BOVIN	Q3MHW2_bos taur
112	314	8.0	855	1	ST14_MOUSE	P66677_mus muscul	185	281	7.1	492	1	FA10_BOVIN	P00743_bos taur
113	314	8.0	855	2	Q543E3_MOUSE	Q543E3_m 0 day neo	186	281	7.1	492	2	Q3TDB9_MOUSE	Q3TDB9_mus musc
114	313	7.9	855	2	Q9JIT7_RAT	Q9JIT7_rattus norv	187	281	7.1	493	2	Q3UJY1_MOUSE	Q3UJY1_m nod-deriv
115	312.5	7.9	685	2	Q32N65_XENLA	Q32N65_xenopus lae	188	280.5	7.1	264	1	CTRL_HUMAN	P40313_homo sapien
116	312	7.9	467	2	Q58L95_OXYMI	Q58L95_oxynanus m	189	280.5	7.1	269	2	Q8LIW0_HUMAN	Q8LIW0_homo sapien
117	311	7.9	446	1	FA7_RAT	Q8K195_rattus norv	190	280	7.1	562	1	TPA_HUMAN	P00750_homo sapien
118	310.5	7.9	434	2	Q7T3B6_BRARE	Q7T3B6_brachydanio	191	278.5	7.1	466	1	FA7_HUMAN	P08709_homo sapien
119	310.5	7.9	453	2	Q58L94_9SAUR	Q58L94_notechis sc	192	278.5	7.1	824	2	Q6TCC2_HUMAN	P08709_homo sapien
120	310.5	7.9	461	1	PROC_HUMAN	P94070_h vitamin k	193	278	7.0	408	2	Q9VW19_DROME	Q9VW19_drosophila
121	310.5	7.9	461	2	Q53E74_HUMAN	Q53E74_homo sapien	194	278	7.0	433	2	Q804X5_CHICK	Q804X5_gallus gall
122	309.5	7.8	689	2	Q4VA78_XENTR	Q4VA78_xenopus tro	195	278	7.0	488	1	FA10_HUMAN	P00742_homo sapien
123	309.5	7.8	799	1	TMPS6_MOUSE	Q4db10_mus muscul	196	278	7.0	488	2	Q5JVE7_HUMAN	Q5JVE7_homo sapien
124	309.5	7.8	811	2	Q3KN88_MOUSE	Q3KN88_mus muscul	197	278	7.0	562	2	Q503B0_HUMAN	Q503B0_homo sapien
125	305	7.7	456	1	PROC_CANPA	Q28278_c vitamin k	198	278	7.0	113	1	CORIN_MOUSE	Q92319_mus musc
126	304	7.7	1069	1	ENTK_MOUSE	P97435_mus muscul	199	277	7.0	559	1	TPA_RAT	P19637_rattus norv
127	302.5	7.7	445	2	Q19A27_PIG	Q19A27_bos scrofa	200	277	7.0	562	2	Q5R8U0_PONPY	Q5R8U0_pongo pygma
128	302.5	7.7	446	1	FA7_MOUSE	P70375_mus muscul	201	276.5	7.0	24	2	Q53FV9_HUMAN	Q53FV9_homo sapien
129	302.5	7.7	446	2	Q542C2_MOUSE	Q542C2_m b6-derivate	202	276.5	7.0	625	2	Q3MER7_BOVIN	Q3MER7_bos taur
130	301.5	7.6	433	2	Q8JHD0_BRARE	Q8JHD0_brachydanio	203	276.5	7.0	655	1	HGFA_HUMAN	Q04756_homo sapien
131	300.5	7.6	463	2	Q6IT10_PSETE	Q6IT10_pseudonaja	204	276.5	7.0	655	2	Q51X47_HUMAN	Q51X47_homo sapien
132	299.5	7.6	433	2	Q504H3_BRARE	Q504H3_brachydanio	205	276.5	7.0	679	2	Q9EPQ8_HUMAN	Q9EPQ8_homo sapien
133	299.5	7.6	467	2	Q6IT09_PSETE	Q6IT09_pseudonaja	206	276	7.0	559	2	Q6P7U0_MOUSE	Q6P7U0_homo sapien
134	299	7.6	1111	2	Q80YN4_RAT	Q80YN4_rattus norv	207	275.5	7.0	444	2	Q5JVF1_MOUSE	Q5JVF1_m plasminog
135	298.5	7.6	433	2	Q90YK1_XENLA	Q90YK1_brachydanio	208	275.5	7.0	498	2	Q4RP66_TETNG	Q4RP66_tetraodon n
136	298.5	7.6	553	2	Q6P719_XENLA	Q6P719_xenopus lae	209	275.5	7.0	655	2	Q2M1W7_HUMAN	Q2M1W7_homo sapien
137	298	7.6	449	2	Q56VR3_PSETE	Q56VR3_pseudonaja	210	275.5	7.0	1134	2	Q7RRY7_HUMAN	Q7RRY7_homo sapien
138	297.5	7.5	777	2	Q8CAN9_MOUSE	Q8CAN9_mus muscul	211	275.5	7.0	3247	2	Q4RCF1_TETNG	Q4RCF1_tetraodon n
139	297.5	7.5	3239	2	Q4S0Y8_TETNG	Q4S0Y8_tetraodon n	212	275	7.0	497	2	Q4SVF9_TETNG	Q4SVF9_tetraodon n
140	297	7.5	456	2	Q5FVZ2_XENTR	Q5FVZ2_xenopus tro	213	275	7.0	1047	2	Q566K6_MOUSE	Q566K6_mus musc
141	297	7.5	459	1	PROC_PIG	Q9G129_r vitamin k	214	274.5	7.0	445	2	Q504J5_BRARE	Q504J5_brachydanio
142	296	7.5	463	2	Q1L658_PSETE	Q1L658_pseudonaja	215	274.5	7.0	547	2	Q5BKN3_XENTR	Q5BKN3_xenopus tro
143	296	7.5	458	1	PROC_RABIT	Q28661_o vitamin k	216	274.5	7.0	566	2	Q2KJG9_BOVIN	Q2KJG9_bos taur
144	296	7.5	485	2	Q4VA71_XENTR	Q4VA71_xenopus tro	217	274.5	7.0	625	1	THRB_BOVIN	P00735_bos taur
145	295.5	7.5	336	2	Q8CIR9_MOUSE	Q8CIR9_mus muscul	218	274.5	7.0	654	1	HGFA_CANPA	Q6qnt4_cantis fami
146	295.5	7.5	441	2	Q804X2_FUGRU	Q804X2_fugu rubrip	219	274.5	7.0	1235	2	Q659T9_CIOIN	Q659T9_ciona intes
147	295.5	7.5	505	2	Q4SB52_TETNG	Q4SB52_tetraodon n	220	274.5	7.0	3670	1	Q8JHC9_HUMAN	Q7Z407_homo sapien
148	295	7.5	425	2	Q804X7_CHICK	Q804X7_gallus gall	221	273.5	6.9	443	2	Q8JHC9_BRARE	Q8JHC9_brachydanio
149	294	7.5	364	2	Q68FY8_RAT	Q68FY8_rattus norv	222	273.5	6.9	466	1	FA7_PANTR	Q2F992_pan troglod
150	293.5	7.4	364	2	Q4G030_RAT	Q4G030_rattus norv	223	273.5	6.9	517	2	Q3VU8_MOUSE	Q3VU8_mus musc
151	293.5	7.4	446	2	Q38J75_CANPA	Q38J75_cantis fami	224	273.5	6.9	566	1	TPA_BOVIN	Q28198_bos taur
152	293.5	7.4	447	1	FA7_BOVIN	P22457_bos taurus	225	273	6.9	394	2	Q5S1X0_IXOSC	Q5S1X0_ixodes scap
153	293.5	7.4	1331	2	Q4S572_TETNG	Q4S572_tetraodon n	226	273	6.9	507	2	Q1RLV2_BRARE	Q1RLV2_brachydanio
154	293	7.4	430	2	Q804X0_FUGRU	Q804X0_fugu rubrip	227	273	6.9	560	1	HABP2_HUMAN	Q14530_h_hyalurona
155	292	7.4	461	1	PROC_RAT	P11394_r vitamin k	228	273	6.9	2796	1	CSMD3_MOUSE	Q80C79_mus musc
156	291.5	7.4	390	2	Q69DJ3_PIG	Q69DJ3_bos scrofa	229	273	6.9	2972	2	Q4SIZ1_TETNG	Q4SIZ1_tetraodon n
157	291	7.4	475	2	Q804W9_FUGRU	Q804W9_fugu rubrip	230	272.5	6.9	321	2	Q6WZL2_HUMAN	Q6WZL2_homo sapien
158	290.5	7.4	479	2	Q19A26_PIG	Q19A26_bos scrofa	231	272.5	6.9	466	1	FA7_PANPA	Q2F994_pan paniscu
159	290	7.4	464	2	Q5FW21_XENTR	Q5FW21_xenopus tro	232	271.5	6.9	244	1	KLKE_HUMAN	Q92876_homo sapien
160	289.5	7.3	466	1	FA9_FELCA	Q6ea95_felis silve	233	271.5	6.9	244	2	Q6H3J1_HUMAN	Q6H3J1_homo sapien
161	287.5	7.3	802	1	TMPS6_HUMAN	Q6tue8_homo sapien	234	271.5	6.9	461	1	Q6TBE4_RAT	Q6TBE4_rattus norv
162	287.5	7.3	980	2	Q6ETN7_BURAR	Q6ETN7_bufo arenar	235	271	6.9	433	2	Q8MIL0_RABIT	Q8MIL0_oryctolagus
163	287	7.3	467	2	Q58L96_SSAUR	Q58L96_oxynanus s	236	271	6.9	433	2	Q8MHY7_RABIT	Q8MHY7_oryctolagus
164	287	7.3	504	2	Q4V971_BRARE	Q4V971_brachydanio	237	271	6.9	559	2	TPA_MOUSE	P11214_mus muscul
165	285.5	7.2	452	1	FA9_CANPA	P19540_cantis fami	238	270.5	6.9	375	2	Q5WIK5_NILLU	Q5WIK5_nilaparvata
166	285	7.2	504	2	Q6PGW7_BRARE	Q6PGW7_brachydanio	239	270.5	6.9	1022	2	Q4T9V1_TETNG	Q4T9V1_tetraodon n
167	284	7.2	432	2	Q6GNA2_XENLA	Q6GNA2_xenopus lae	240	270	6.8	477	1	URR1_DESRO	P98119_desmodus ro
168	284	7.2	974	2	Q90W88_BURFA	Q90W88_bufo japoni	241	270	6.8	490	1	FA10_RABIT	P19045_oryctolagus
169	283.5	7.2	482	1	FA10_RAT	Q63207_rattus norv	242	269	6.8	261	2	Q6DHD9_BRARE	Q6DHD9_brachydanio
170	283.5	7.2	589	2	Q6PJ45_HUMAN	Q6PJ45_homo sapien	243	269	6.8	265	2	Q56IU4_BRARE	Q56IU4_brachydanio
171	283	7.2	376	1	FA10_HOPEST	P83370_hoplostcephal	244	269	6.8	643	2	Q97506_PIG	Q97506_bos scrofa
172	282.5	7.2	320	2	Q8CIR7_RAT	Q8CIR7_rattus norv	245	269	6.8	833	2	Q96442_STRBU	Q96442_strongyloce
173	282.5	7.2	666	2	Q2KJ63_BOVIN	Q2KJ63_bos taur	246	268.5	6.8	290	2	Q58E07_XENLA	Q58E07_xenopus lae
174	282	7.1	456	1	PROC_BOVIN	P00745_b vitamin k	247	268	6.8	538	1	HABP2_BOVIN	Q5e922_b_hyalurona
175	282	7.1	469	2	Q9GMD9_ORNAN	Q9GMD9_ornithorhyn	248	268	6.8	558	2	Q3MHR6_BOVIN	Q3MHR6_bos taur
176	282	7.1	1466	2	Q7ZZ41_BRARE	Q7ZZ41_brachydanio	249	268	6.8	740	2	Q4TB33_TETNG	Q4TB33_tetraodon n
177	282	7.1	3417	2	Q1L898_BRARE	Q1L898_brachydanio	250	267.5	6.8	268	2	Q6GQ99_XENLA	Q6GQ99_xenopus lae

251	267	6.8	455	2	075x86_XENLA	075x86 xenopus lae	324	255.5	6.5	359	2	028xR0_DROPS	028xR0 drosophila
252	267	6.8	463	2	05M8Y0_XENTR	05M8Y0 xenopus tro	325	255.5	6.5	587	2	017FW1_AEDAE	017FW1 aedes aegypt
253	267	6.8	868	2	09Y1V3_POLMI	09Y1V3 polyanthrocra	326	255.5	6.5	763	2	031430_LAMJA	031430 lampectra ja
254	266.5	6.8	441	2	04SU02_TETNG	04SU02 tetraodon n	327	255	6.5	325	2	015944_SARPE	015944 sarcoptahaga
255	266	6.7	352	2	07KVM3_DROME	07KVM3 drosophila	328	255	6.5	845	2	06GR54_XENLA	06GR54 xenopus lae
256	266	6.7	359	2	017FW0_AEDAE	017FW0 aedes aegypt	329	254.5	6.5	250	2	028YV4_DROPS	028YV4 drosophila
257	266	6.7	359	2	04SU09_TETNG	04SU09 tetraodon n	330	254.5	6.5	315	2	07TT44_MOUSE	07TT44 mus musculu
258	266	6.7	889	2	05GCC1_CARPO	05GCC1 carcinoscor	331	254.5	6.5	461	2	09SND6_PANTR	09SND6 pan troglod
259	265.5	6.7	250	2	09Y514_DROME	09Y514 drosophila	332	254	6.4	314	2	09VR15_DROME	09VR15 drosophila
260	265.5	6.7	264	2	04SEW3_TETNG	04SEW3 tetraodon n	333	254	6.4	617	1	THRB_RAT	THRB ratu
261	265	6.7	311	2	050214_BRARE	050214 brachydantio	334	254	6.4	998	2	05H875_CIOIN	05H875 cioin
262	265	6.7	381	2	029DF3_DROPS	029DF3 drosophila	335	253.5	6.4	471	2	03UES1_MOUSE	03UES1 mus musculu
263	265	6.7	045U7	2	04SU07_TETNG	045U7 tetraodon n	336	253.5	6.4	487	2	09NZP8_HUMAN	09NZP8 homo sapien
264	264.5	6.7	431	1	URTB_DESRO	p98121 desmodus ro	337	253.5	6.4	615	2	06GNK4_XENLA	06GNK4 xenopus lae
265	264.5	6.7	618	1	THRB_MOUSE	p19221 mus musculu	338	253.5	6.4	628	2	09VER6_DROME	09VER6 drosophila
266	264.5	6.7	618	1	03T094_MOUSE	03T094 mus musculu	339	253	6.4	263	2	04SEW1_TETNG	04SEW1 tetraodon n
267	264	6.7	653	1	HGFA_MOUSE	09R098 mus musculu	340	253	6.4	471	1	FA9_CHICK	FA9 gallu
268	264	6.7	653	1	0545J3_MOUSE	0545J3 m 10 day ol	341	253	6.4	616	1	FA12_PIG	FA12 aplysia cal
269	264	6.7	653	1	05EBA7_RAT	05EBA7 rattus norv	342	253	6.4	1070	2	P91972_APICA	P91972 sparus aura
270	264	6.7	910	2	04RRD7_TETNG	04RRD7 tetraodon n	343	252.5	6.4	241	2	04QY79_SPRAU	04QY79 sparus aura
271	263.5	6.7	253	2	07SX97_BRARE	07SX97 brachydantio	344	252.5	6.4	487	2	053GX9_HUMAN	053GX9 homo sapien
272	263.5	6.7	444	2	02F9N5_PONPY	02F9N5 pongo pygma	345	252	6.4	260	2	06E2V9_XENTR	06E2V9 xenopus tro
273	263.5	6.7	444	2	02F9N4_PONPY	02F9N4 pongo pygma	346	252	6.4	261	2	066HW9_BRARE	066HW9 brachydantio
274	263	6.7	431	2	05SWW9_HUMAN	05SWW9 homo sapien	347	252	6.4	600	2	05R976_PONPY	05R976 pongo pygma
275	263	6.7	431	2	053XS3_HUMAN	053XS3 homo sapien	348	252	6.4	607	2	06DRJ5_XENLA	06DRJ5 xenopus lae
276	263	6.7	653	2	08VCS4_MOUSE	08VCS4 mus musculu	349	251.5	6.4	267	2	07RG94_ANOGA	07RG94 anopheles g
277	263	6.7	3239	2	04SIT9_TETNG	04SIT9 tetraodon n	350	251.5	6.4	389	2	0177F1_AEDAE	0177F1 aedes aegypt
278	262.5	6.7	300	2	0819P4_AURAU	0819P4 aurelia aur	351	251	6.4	263	2	051029_XENTR	051029 xenopus tro
279	262.5	6.7	461	1	FA9_HUMAN	P00740 homo sapien	352	251	6.4	295	2	08CIP7_RAT	08CIP7 rattus norv
280	262.5	6.7	461	1	FA9_PANTR	09SND7 pan troglod	353	251	6.4	343	2	0504K1_BRARE	0504K1 brachydantio
281	262.5	6.7	461	2	05YJ88_HUMAN	05YJ88 homo sapien	354	251	6.4	407	2	07OKL1_ANOGA	07OKL1 anopheles g
282	262.5	6.7	1042	2	CORIN_HUMAN	09Y545 homo sapien	355	251	6.4	537	2	0804W8_FUGRU	0804W8 fugu rubrip
283	262.5	6.7	1042	2	02TBD2_HUMAN	02TBD2 homo sapien	356	251	6.4	969	2	02ABP0_BRARE	02ABP0 brachydantio
284	262	6.6	314	2	029LAI_DROPS	029LAI drosophila	357	251	6.4	1215	2	04H2P2_CIOIN	04H2P2 cioin
285	262	6.6	477	1	UR12_DESRO	P15638 desmodus ro	358	251	6.4	1378	2	028YJ3_DROPS	028YJ3 drosophila
286	262	6.6	653	2	03T0U8_MOUSE	03T0U8 mus musculu	359	250.5	6.3	347	1	HPT_RABIT	P19087 oryctolagus
287	262	6.6	284	2	08AXO8_XENLA	08AXO8 xenopus lae	360	250.5	6.3	548	2	0502D2_BRARE	0502D2 brachydantio
288	261.5	6.6	442	1	UROK_PIG	P04185 sus scrofa	361	250.5	6.3	875	1	NERR_PANTR	NERR pan troglod
289	261	6.6	431	1	UROK_HUMAN	P00749 h urokinase	362	250	6.3	263	2	01UPZ1_BRARE	01UPZ1 brachydantio
290	261	6.6	433	1	UROK_BOVIN	P00559 bos taurus	363	250	6.3	303	1	BSSP4_MOUSE	BSSP4 mus musculu
291	261	6.6	969	2	05K0U1_MACPA	05K0U1 macaca fasc	364	250	6.3	562	2	08S023_PIG	08S023 sus scrofa
292	260.5	6.6	264	2	09EQZ8_RAT	09EQZ8 rattus norv	365	250	6.3	845	2	0632O6_XENLA	0632O6 xenopus lae
293	260.5	6.6	456	2	07T143_MOUSE	07T143 mus musculu	366	250	6.3	1379	2	09VAN6_DROME	09VAN6 drosophila
294	260.5	6.6	462	2	06PAG2_XENLA	06PAG2 xenopus lae	367	250	6.3	1397	2	07KQO9_DROME	07KQO9 drosophila
295	260.5	6.6	482	2	03UZO9_MOUSE	03UZO9 mus musculu	368	249.5	6.3	303	2	016NA7_AEDAE	016NA7 aedes aegypt
296	260.5	6.6	482	2	03VO19_MOUSE	03VO19 mus musculu	369	249.5	6.3	400	2	027081_TACTR	027081 tachypleus
297	260.5	6.6	1042	2	05K0U3_MACPA	05K0U3 macaca fasc	370	249.5	6.3	430	2	01RLR1_BRARE	01RLR1 brachydantio
298	260	6.6	431	2	05R929_PONPY	05R929 pongo pygma	371	249.5	6.3	435	2	04TBY8_TETNG	04TBY8 tetraodon n
299	259	6.6	245	1	CTRB_GADMO	P80646 gadus morhu	372	249.5	6.3	552	2	011029_BRARE	011029 brachydantio
300	259	6.6	416	1	FA9_BOVIN	P00741 bos taurus	373	249.5	6.3	875	1	NERR_HUMAN	NERR homo sapien
301	259	6.6	474	2	08JHC8_BRARE	08JHC8 brachydantio	374	249	6.3	263	2	06GPT1_HUMAN	06GPT1 homo sapien
302	259	6.6	581	2	09XZM7_STRPU	09XZM7 strongyloce	375	249	6.3	263	2	09CR35_MOUSE	09CR35 mus musculu
303	259	6.6	1005	2	05K0U2_MACPA	05K0U2 macaca fasc	376	249	6.3	328	2	03UEP7_MOUSE	03UEP7 mus musculu
304	258.5	6.6	255	2	07QCS5_ANOGA	07QCS5 anopheles g	377	249	6.3	409	1	FA9_PIG	FA9 su
305	258.5	6.6	411	2	05PY49_HUMAN	05PY49 homo sapien	378	248.5	6.3	548	2	05MB55_MANSE	05MB55 manduca sex
306	258.5	6.6	787	1	STUR_DROME	09SPW6 gadus morhu	379	248.5	6.3	241	2	04Q773_SPRAU	04Q773 sparus aura
307	258	6.5	253	2	09PM06_GADMO	09PM06 gadus morhu	380	248.5	6.3	401	2	04R883_TETNG	04R883 tetraodon n
308	258	6.5	342	2	017PZ2_AEDAE	017PZ2 aedes aegypt	381	248.5	6.3	623	2	019A28_PIG	019A28 sus scrofa
309	258	6.5	433	1	UROK_PAPCY	05P227 p urokinase	382	248.5	6.3	459	2	019A28_PIG	019A28 sus scrofa
310	258	6.5	612	2	0804W7_MANSE	0804W7 manduca sex	383	248.5	6.3	744	2	070137_ANOGA	070137 anopheles g
311	258	6.5	644	2	05MPB9_FUGRU	05MPB9 fugu rubrip	384	248.5	6.3	876	1	NERR_GORGO	05G970 gorilla gor
312	257.5	6.5	580	2	0501G7_ORYLA	0501G7 oryzae lat	385	248	6.3	259	2	06A2C2_BRARE	06A2C2 brachydantio
313	257.5	6.5	607	2	04Q853_XENLA	04Q853 xenopus lae	386	248	6.3	261	2	09W7Q4_PAROL	09W7Q4 paralicthy
314	257.5	6.5	680	2	0294V2_DROPS	0294V2 drosophila	387	248	6.3	263	1	CTRB1_HUMAN	09W7Q4 paralicthy
315	257.5	6.5	1004	2	079953_XENLA	079953 xenopus lae	388	248	6.3	540	2	0800Y7_MEIGA	0800Y7 meiga
316	257	6.5	273	2	070812_ANOGA	070812 anopheles g	389	248	6.3	570	2	017PV4_AEDAE	017PV4 aedes aegypt
317	257	6.5	607	2	05FW1_XENTR	05FW1 xenopus tro	390	248	6.3	638	1	KIKX1_HUMAN	KIKX1 homo sapien
318	257	6.5	999	2	05H876_CIOIN	05H876 cioin	391	248	6.3	638	2	04M5C3_HUMAN	04M5C3 homo sapien
319	256.5	6.5	264	2	09DP78_MOUSE	09DP78 mus musculu	392	248	6.3	638	2	017RE9_HUMAN	017RE9 homo sapien
320	256.5	6.5	264	2	09ER05_MOUSE	09ER05 mus musculu	393	248	6.3	638	1	017RE8_HUMAN	017RE8 homo sapien
321	256.5	6.5	453	2	04SU01_TETNG	04SU01 tetraodon n	394	248	6.3	764	1	CFAB_PANTR	0864W8 pan troglod
322	256	6.5	243	2	07PWE3_ANOGA	07PWE3 anopheles g	395	248	6.3	775	2	06P550_MOUSE	06P550 mus musculu
323	255.5	6.5	268	2	064288_XENTR	064288 xenopus tro	396	248	6.3	991	2	06NZM2_MOUSE	06NZM2 mus musculu

397	248	6.3	1469	2	Q29B27_DROPS	Q29b27_drosophila	470	242	6.1	725	2	Q4SGT4_TETNG	Q4sgt4_tetradon n
398	247.5	6.3	307	2	Q7TMC0_MOUSE	Q7tmc0_mus musculus	471	241.5	6.1	269	2	Q4S850_TETNG	Q4s850_tetradon n
399	247.5	6.3	311	2	Q9WLC2_DROME	Q9wlc2_drosophila	472	241.5	6.1	279	2	Q9WSM4_MOUSE	Q9wsM4_mus musculus
400	247.5	6.3	991	1	BMPI_MOUSE	P88063_mus musculus	473	241.5	6.1	279	2	Q3M154_MOUSE	Q3m154_mus musculus
401	247	6.3	235	2	Q28731_RABIT	Q28731_oryctolagus	474	241.5	6.1	416	2	Q86T26_HUMAN	Q86t26_homo sapien
402	247	6.3	275	1	TRYT_CANFA	P15944_canis famil	475	241.5	6.1	623	1	THR8_PONPY	Q51537_pongo pygma
403	247	6.3	364	2	Q917V4_DROME	Q917v4_drosophila	476	241.5	6.1	875	1	NETR_SAGLB	Q5g265_sagallius la
404	247	6.3	386	2	O81924_BOMMO	O81924_bombyx mori	477	241.5	6.1	875	1	NETR_TRAPH	Q5g265_tachypithe
405	247	6.3	764	1	CPAB_HUMAN	P00751_homo sapien	478	241	6.1	296	2	Q5FV77_XENTR	Q5fV77_xenopus tro
406	247	6.3	764	2	O5JPE7_HUMAN	O5jpe7_homo sapien	479	241	6.1	346	1	HPT_MESAU	Q35086_mesocricetu
407	247	6.3	764	2	O5JFE9_HUMAN	O5jfe9_homo sapien	480	241	6.1	818	2	O6PBA6_BRARE	Q6pba6_brachydantio
408	247	6.3	764	2	O5ST50_HUMAN	Q5st50_homo sapien	481	241	6.1	862	2	Q7Q058_ANOCA	Q7q058_anopheles g
409	247	6.3	986	1	BMPI_HUMAN	Q34550_homo sapien	482	241	6.1	1415	2	Q8MJ16_BOVIN	Q8mj16_bos taurus
410	246.5	6.2	235	2	Q90387_CYNPY	Q90387_cynops pyr	483	240.5	6.1	238	2	Q9W706_PAROL	Q9w706_parallelchi
411	246.5	6.2	264	2	Q9D960_MOUSE	Q9d960_mus musculus	484	240.5	6.1	266	2	Q4QY80_SPAU	Q4qy80_sparus aura
412	246.5	6.2	297	2	O88781_RATRT	O88781_rattus ratc	485	240.5	6.1	366	2	Q2T9Y2_BOVIN	Q2t9y2_bos taurus
413	246.5	6.2	335	2	Q4T7B2_TETNG	Q4t7e2_tetradon n	486	240.5	6.1	422	2	O8WVC1_HUMAN	Q8wvc1_homo sapien
414	246.5	6.2	347	1	HPT_ATEGE	P50417_ateles geof	487	240.5	6.1	3548	2	O5VTE4_HUMAN	Q5vte4_homo sapien
415	246.5	6.2	418	2	Q4R6T2_MACFA	Q4r6t2_macaca fasc	488	240	6.1	242	2	Q92099_PARGG	Q92099_parmotoche
416	246.5	6.2	486	2	O5PRA6_BRARE	O5pra6_brachydantio	489	240	6.1	1059	2	TMPS9_HUMAN	Q72410_homo sapien
417	246.5	6.2	622	1	THRB_HUMAN	P00734_homo sapien	490	239.5	6.1	240	2	O98TH0_9TELE	Q98th0_engraulae j
418	246.5	6.2	622	1	Q4QZ50_HUMAN	Q4qz40_homo sapien	491	239.5	6.1	371	2	O5MPC6_MANSE	Q5mpc6_manduca sex
419	246.5	6.2	622	2	O53H06_HUMAN	Q53h06_homo sapien	492	239.5	6.1	406	1	HPT_HUMAN	P00738_homo sapien
420	246.5	6.2	622	2	O53H04_HUMAN	Q53h04_homo sapien	493	239.5	6.1	1015	2	Q2M1H1_HUMAN	Q2m1h1_homo sapien
421	246.5	6.2	622	2	O7Z7P3_HUMAN	Q7z7p3_homo sapien	494	239.5	6.1	1015	2	Q2MIH1_HUMAN	Q2mi11_homo sapien
422	246	6.2	249	2	O5TNA8_ANOCA	O5tna8_anopheles g	495	239.5	6.1	3567	2	O9ES77_MOUSE	Q9es77_mus musculus
423	246	6.2	263	2	Q9D8X8_MOUSE	Q9d8x8_mus musculus	496	239	6.1	245	1	CTRA_BOVIN	P00766_bos taurus
424	246	6.2	267	2	O5BK00_XENTR	Q5bk00_xenopus tro	497	239	6.1	264	2	Q4QY78_SPAU	Q4qy78_sparus aura
425	246	6.2	764	1	CPAB_BOVIN	Q64649_gorilla gor	498	239	6.1	268	2	Q4PZ03_ANOCA	Q4pZ03_anopheles g
426	246	6.2	812	1	PLMN_GOING	Q68668_bos taurus	499	239	6.1	335	2	Q2AAD0_PHACA	Q2aad0_phalaecrocor
427	245.5	6.2	265	2	O804G1_BRARE	O804g1_brachydantio	500	239	6.1	435	2	O7QC30_ANOCA	Q7qc30_anopheles g
428	245.5	6.2	467	2	Q967X8_PANAR	Q967x8_pannulus a	501	239	6.1	436	1	HEPS_MOUSE	Q35433_mus musculus
429	245	6.2	263	2	O6GNF7_XENLA	O6gnf7_xenopus lae	502	239	6.1	638	2	O5FV52_RAT	O5fV52_rattus norv
430	245	6.2	277	2	Q7PKB8_ANOCA	Q7pkb8_anopheles g	503	239	6.1	977	2	O91925_XENLA	Q91925_xenopus lae
431	245	6.2	369	2	Q2VGB6_BOMMO	Q2vgb6_bombyx mori	504	238.5	6.0	268	2	O46151_PACIE	Q46151_pactiaetacu
432	245	6.2	638	2	O8R0P5_MOUSE	Q8r0p5_mus musculus	505	238.5	6.0	578	2	Q6Q0I7_BOVIN	Q6q0i7_bos taurus
433	245	6.2	639	1	BMPI_STRPU	P88063_strongyloce	506	238.5	6.0	625	1	FALL_BOVIN	Q5nct3_bos taurus
434	245	6.2	1167	2	O5T6B6_HUMAN	O5t6b6_homo sapien	507	238.5	6.0	928	2	Q7QAH1_ANOCA	Q7qah1_anopheles g
435	244.5	6.2	223	2	Q4QY74_SPAU	Q4qy74_sparus aura	508	238	6.0	237	1	TRYP_ASTRF	P00761_atactus flu
436	244.5	6.2	242	2	Q7Q9W3_ANOCA	Q7q9w3_anopheles g	509	238	6.0	242	2	Q1AMP9_DISMA	Q1amp9_dissotichu
437	244.5	6.2	511	2	O570Z4_MOUSE	O570z4_mus musculus	510	238	6.0	263	3	CTR2_CANFA	Q9n2d1_canis famil
438	244.5	6.2	608	2	Q9PTW7_STRCA	Q9ptw7_struthio ca	511	238	6.0	275	1	TRYT_PIG	O9n2d1_sus scrofa
439	244.5	6.2	1061	1	TMPS9_RAT	P65922_rattus norv	512	238	6.0	283	2	Q7PY20_ANOCA	Q7py20_anopheles g
440	244	6.2	263	2	Q9DC86_MOUSE	Q9dc86_mus musculus	513	238	6.0	347	1	HPT_PONPY	O5f566_pongo pygma
441	244	6.2	311	2	O1IV42_BRARE	O1iv42_brachydantio	514	238	6.0	375	1	PCE_TACTR	P21992_tachypiteus
442	244	6.2	322	2	Q920S2_MOUSE	Q920s2_mus musculus	515	238	6.0	435	2	O9NFE2_ANOCA	Q9nfe2_anopheles g
443	244	6.2	445	2	Q3U0U6_MOUSE	Q3u0u6_mus musculus	516	238	6.0	767	2	Q9DGR2_XENLA	Q9dgr2_xenopus lae
444	244	6.2	638	1	KLKB1_MOUSE	P26262_mus musculus	517	237.5	6.0	251	2	O171W0_AEDAE	Q171w0_aedes aegy
445	244	6.2	986	2	Q2ABP1_BRARE	Q2abp1_brachydantio	518	237.5	6.0	267	2	Q4QRF8_BRARE	Q4qrF8_brachydantio
446	244	6.2	1806	2	O571B7_MOUSE	O571b7_mus musculus	519	237.5	6.0	371	2	O177B4_AEDAE	Q177b4_aedes aegy
447	243.5	6.2	285	2	O8CG42_RAT	O8cg42_rattus norv	520	237.5	6.0	449	2	Q7PY21_AEDAE	Q7py21_aedes aegy
448	243.5	6.2	435	2	SNAK_DROME	P05045_drosophila	521	237.5	6.0	475	2	Q3T206_MOUSE	Q3t206_mus musculus
449	243.5	6.2	435	2	Q290H0_DROME	Q290h0_drosophila	522	237.5	6.0	607	2	Q297J7_DROPS	Q297j7_drosophila
450	243.5	6.2	555	2	O5FVX1_XENTR	O5fvx1_xenopus tro	523	237.5	6.0	735	2	O57381_XENLA	O57381_xenopus lae
451	243.5	6.2	764	1	CPAB_PONPY	O66441_pongo pygma	524	237.5	6.0	735	2	O66K13_XENLA	O66k13_xenopus lae
452	243.5	6.2	877	1	NETR_PONPY	O52629_pongo pygma	525	237.5	6.0	810	1	PLMN_ERIEU	Q29445_eritaceus e
453	243	6.2	261	2	Q4RHR8_TETNG	Q4rhr8_tetradon n	526	237	6.0	237	2	Q91515_FUGRU	Q91515_fugu rubrip
454	243	6.2	273	1	TRYT_SHEEP	Q9xsm2_ovis aries	527	237	6.0	263	1	CTRBI_RAT	P07338_rattus norv
455	243	6.2	331	2	Q16G06_AEDAE	Q16g06_aedes aegy	528	237	6.0	263	2	Q6PGS4_XENLA	Q6pgs4_xenopus lae
456	243	6.2	442	2	O804X1_FUGRU	Q804x1_fugu rubrip	529	237	6.0	963	2	Q5H874_CIOIN	Q5h874_ciona lites
457	242.5	6.1	233	2	Q4RV18_TETNG	Q4rv18_tetradon n	530	236.5	6.0	227	2	Q7QD79_ANOCA	Q7qd79_anopheles g
458	242.5	6.1	279	2	Q3JUN5_MOUSE	Q3jun5_mus musculus	531	236.5	6.0	248	2	Q28X04_DROPS	Q28x04_drosophila
459	242.5	6.1	564	2	O8MKR1_RABIT	O8mkr1_oryctolagus	532	236.5	6.0	251	2	Q7Q9W2_ANOCA	Q7q9w2_anopheles g
460	242.5	6.1	564	2	Q5R502_PONPY	O5r502_pongo pygma	533	236.5	6.0	274	1	MCPT6_RAT	P50342_rattus norv
461	242.5	6.1	574	2	Q8RLR8_9CAEN	Q8rlr8_ilyanassa o	534	236.5	6.0	707	1	Q29BPS_DROPS	Q29bps_drosophila
462	242.5	6.1	578	2	Q17GV5_AEDAE	Q17gv5_aedes aegy	535	236.5	6.0	707	1	BMPI_XENLA	P98070_xenopus lae
463	242.5	6.1	891	2	O57658_CHICK	O57658_gallus galli	536	236.5	6.0	761	2	Q9JVC8_RAT	Q9jvc8_rattus norv
464	242.5	6.1	893	2	O59F71_HUMAN	O59f71_homo sapien	537	236.5	6.0	1013	1	TLI1_MOUSE	Q62381_mus musculus
465	242.5	6.1	875	1	NETR_HYLLE	O52626_hyllobates l	538	236	6.0	267	2	Q7QAK5_ANOCA	Q7qak5_anopheles g
466	242.5	6.1	875	1	NETR_MACNU	O52626_macaca mula	539	236	6.0	328	2	Q5BL24_BRARE	Q5bl24_brachydantio
467	242.5	6.1	1019	1	TLI2_XENLA	O57382_xenopus lae	540	236	6.0	519	2	O5MG68_LONON	Q5mg68_lionomia obi
468	242.5	6.1	1065	1	TMPS9_MOUSE	P65925_mus musculus	541	236	6.0	812	1	PLMN_MOUSE	P20918_mus musculus
469	242.5	6.1	3574	2	Q4LDB5_HUMAN	Q4ldes_homo sapien	542	236	6.0	1550	2	Q4T392_TETNG	Q4t392_tetradon n

543	235.5	6.0	259	2	Q50BF4_9DIPT	050b4 culicoides	616	230	5.8	372	2	Q9Y1K6_ANOGA	Q9Y1K6 anopheles g
544	235.5	6.0	260	2	Q9W703_PAROL	Q9W703 paratichthy	617	230	5.8	607	2	Q91001_CHICK	Q91001 gallus gall
545	235.5	6.0	359	2	Q6AXZ6_RAT	Q6AXZ6 rattus norv	618	229.5	5.8	235	2	Q19WT4_BUBBU	Q19WT4 bubalus bub
546	235.5	6.0	433	2	Q812A6_MOUSE	Q812A6 mus musculu	619	229.5	5.8	329	1	HPT CANFA	P19006 canis famli
547	235.5	6.0	734	2	Q28C16_XENTR	Q28C16 xenopus tiro	620	229.5	5.8	374	2	Q9VUG2_DROME	Q9VUG2 drosophila
548	235	6.0	261	2	Q4QY77_SPAUV	Q4QY77 sparus aura	621	229.5	5.8	514	2	Q16N50_AEDAE	Q16N50 aedes aegypt
549	235	6.0	270	1	TRYT_MERUN	P50342 meriones un	622	229.5	5.8	624	1	FALL MOUSE	Q91447 mus musculu
550	235	6.0	322	2	Q16Y45_AEDAE	Q16Y45 aedes aegypt	623	229	5.8	267	2	Q9BK47_9ECHI	Q9BK47 luigia foli
551	235	6.0	336	2	Q7RTY5_HUMAN	Q7RTY5 homo sapien	624	229	5.8	274	2	Q3UN30_MOUSE	Q3UN30 mus musculu
552	235	6.0	345	2	Q28B00_PANTR	Q28B00 pan troglod	625	229	5.8	274	2	Q924N9_MOUSE	Q924N9 mus musculu
553	235	6.0	524	2	Q7SXH8_BRARE	Q7SXH8 brachydanio	626	229	5.8	490	2	Q3UKES3_MOUSE	Q3UKES3 mus musculu
554	235	6.0	622	2	Q5NKF9_ONCMY	Q5NKF9 oncorhynch	627	229	5.8	732	2	Q6NWF5_XENIA	Q6NWF5 xenopus lae
555	235	6.0	812	1	PLMN_RAT	Q01177 rattus norv	628	229	5.8	723	2	Q9WTV9_DROME	Q9WTV9 drosophila
556	235	6.0	812	1	Q5BK66_RAT	Q5BK66 rattus norv	629	229	5.8	845	2	Q9DGR1_XENIA	Q9DGR1 xenopus lae
557	235	6.0	1420	1	APQA_MACMU	P14417 macaca mula	630	228.5	5.8	347	2	Q63927_9MURI	Q63927 mus sp. hap
558	234.5	5.9	259	2	Q4S849_TETNG	Q4S849 tetraodon n	631	228.5	5.8	352	2	Q6UBM4_HUMAN	Q6UBM4 homo sapien
559	234.5	5.9	267	2	Q561U9_BRARE	Q561U9 brachydanio	632	228.5	5.8	446	2	Q2TUC1_9DIPT	Q2TUC1 phlebotomus
560	234.5	5.9	271	2	Q5R1Z2_BRARE	Q5R1Z2 brachydanio	633	228.5	5.8	573	2	Q7PV58_ANOGA	Q7PV58 anopheles g
561	234.5	5.9	291	2	Q175R9_AEDAE	Q175R9 aedes aegypt	634	228.5	5.8	600	2	Q17490_ANOGA	Q17490 anopheles g
562	234.5	5.9	300	2	Q175S0_AEDAE	Q175S0 aedes aegypt	635	228.5	5.8	761	2	Q2KTU6_BOVIN	Q2KTU6 bos taurus
563	234.5	5.9	326	2	Q32PT2_BRARE	Q32PT2 brachydanio	636	228.5	5.8	1084	2	Q9BP40_HAIRO	Q9BP40 halocynthia
564	234.5	5.9	375	2	Q2M165_DROPS	Q2M165 anopheles g	637	228.5	5.8	2516	2	Q7T052_MOUSE	Q7T052 mus musculu
565	234.5	5.9	382	2	Q7Q432_ANOGA	Q7Q432 anopheles g	638	228.5	5.8	2566	2	Q7T051_MOUSE	Q7T051 mus musculu
566	234.5	5.9	395	2	Q9BZM1_HUMAN	Q9BZM1 homo sapien	639	228.5	5.8	2531	1	NOTC1_MOUSE	Q01705 mus musculu
567	234.5	5.9	418	2	Q6NPO2_DROME	Q6NPO2 drosophila	640	228.5	5.8	2531	2	Q8K426_MOUSE	Q8K426 mus musculu
568	234.5	5.9	453	1	TMPS3_MOUSE	Q8K10 mus musculu	641	228.5	5.8	2531	2	Q7T050_MOUSE	Q7T050 mus musculu
569	234.5	5.9	453	1	Q2M1G4_MOUSE	Q2M1G4 mus musculu	642	228	5.8	263	2	Q5H2D0_XENTR	Q5H2D0 xenopus tiro
570	234.5	5.9	624	2	Q9DAT3_MOUSE	Q9DAT3 mus musculu	643	228	5.8	3687	2	Q9W332_DROME	Q9W332 drosophila
571	234	5.9	417	1	DESC4_RAT	Q5Q8K2 rattus norv	644	227.5	5.8	235	2	Q91004_GECKO	Q91004 gekko gekko
572	234	5.9	575	2	Q8IRB8_DROME	Q8IRB8 drosophila	645	227.5	5.8	242	1	TRVY_SALSA	P35031 salmo salar
573	234	5.9	573	1	CUBN_MOUSE	Q9J1L4 mus musculu	646	227.5	5.8	251	1	KLK14_HUMAN	Q9PG3 homo sapien
574	233.5	5.9	263	1	CTRA_GADMO	P47796 gadus morhu	647	227.5	5.8	251	2	Q6B089_HUMAN	Q6B089 homo sapien
575	233.5	5.9	267	1	Q7S251_BRARE	Q7S251 brachydanio	648	227.5	5.8	251	2	Q1RMZ2_HUMAN	Q1RMZ2 homo sapien
576	233.5	5.9	450	2	Q90504_EPTST	Q90504 eptatretus	649	227.5	5.8	349	2	Q28802_PATNR	Q28802 pan troglod
577	233.5	5.9	553	2	Q16FY2_AEDAE	Q16FY2 aedes aegypt	650	227.5	5.8	418	2	Q6R15_RAT	Q6R15 rattus norv
578	233.5	5.9	769	2	Q4SC10_TETNG	Q4SC10 tetraodon n	651	227	5.8	249	2	Q6RT79_9LABR	Q6RT79 latocoglabr
579	233	5.9	260	2	Q7Q845_ANOGA	Q7Q845 anopheles g	652	227	5.8	242	2	Q7PKK4_ANOGA	Q7PKK4 anopheles g
580	233	5.9	273	2	Q9XSM1_SHEEP	Q9XSM1 ovis aries	653	227	5.8	263	2	Q7ST54_XENIA	Q7ST54 xenopus lae
581	233	5.9	334	2	Q5MPE9_MANSE	Q5MPE9 manduca sex	654	227	5.8	275	2	Q7YS62_HORSE	Q7YS62 equus cabal
582	233	5.9	366	2	Q2L2S9_DROPS	Q2L2S9 drosophila	655	227	5.8	324	1	TESTR_MOUSE	Q9J1J7 mus musculu
583	233	5.9	445	2	Q8CJ17_RAT	Q8CJ17 rattus norv	656	227	5.8	324	2	Q54AE4_MOUSE	Q54AE4 mus musculu
584	233	5.9	541	2	Q1ED24_BRARE	Q1ED24 brachydanio	657	227	5.8	336	2	Q80YD8_MOUSE	Q80YD8 mus musculu
585	232.5	5.9	485	2	Q5VAN3_PAPHA	Q5VAN3 papio hamad	658	227	5.8	372	2	Q7QKL2_ANOGA	Q7QKL2 anopheles g
586	232.5	5.9	435	2	Q29K17_DROPS	Q29K17 drosophila	659	227	5.8	417	1	DESC4_MOUSE	Q8B510 mus musculu
587	232.5	5.9	936	2	Q81FX2_CRAGI	Q81FX2 crassostrea	660	227	5.8	484	2	Q31IU4_MACMU	Q31IU4 macaca mula
588	232.5	5.9	387	1	Q17FW2_AEDAE	Q17FW2 aedes sapien	661	227	5.8	1464	2	Q9TYH4_SCHMA	Q9TYH4 schistosoma
589	232	5.9	1013	1	TILL1_HUMAN	Q14HP6 bombyx mori	662	227	5.8	1464	2	Q23995_DROME	Q23995 drosophila
590	232	5.9	397	2	Q1HP06_BOMMO	Q05511 rattus norv	663	227	5.8	1464	2	Q24132_DROME	Q24132 drosophila
591	232	5.9	416	1	HEPS_RAT	P14272 rattus norv	664	227	5.8	1464	2	Q9VC47_DROME	Q9VC47 drosophila
592	232	5.9	638	1	KLKBI_RAT	Q3V119 mus musculu	665	226.5	5.7	238	1	TRV3_SALSA	P35033 salmo salar
593	232	5.9	812	2	Q3V119_MOUSE	Q29461 bos taurus	666	226.5	5.7	280	2	Q177F3_AEDAE	Q177F3 aedes aegypt
594	231.5	5.9	269	1	ELAZA2_BOVIN	Q91039 gadus morhu	667	226.5	5.7	371	2	Q8MS52_DROME	Q8MS52 drosophila
595	231.5	5.9	270	2	Q91039_GADMO	Q8CJ16 rattus norv	668	226.5	5.7	761	1	NETR_MOUSE	Q08762 mus musculu
596	231.5	5.9	371	2	Q8CJ16_RAT	Q8CJ16 rattus norv	669	226.5	5.7	1272	2	Q3MTT3_HUMAN	Q3MTT3 homo sapien
597	231.5	5.9	435	2	Q5SMW8_HUMAN	Q5SMW8 homo sapien	670	226.5	5.7	1429	1	ATRN_HUMAN	Q75882 homo sapien
598	231.5	5.9	463	2	Q818X4_DROME	Q818X4 drosophila	671	226	5.7	274	2	Q7PJQ0_ANOGA	Q7PJQ0 anopheles g
599	231.5	5.9	483	2	Q9VK10_DROME	Q9VK10 drosophila	672	226	5.7	394	1	URTG_DESRO	P49150 desmoues ro
600	231.5	5.9	541	2	Q4V875_BRARE	Q4V875 brachydanio	673	226	5.7	416	2	Q4T4R1_TETNG	Q4T4R1 tetraodon n
601	231.5	5.9	603	2	Q5M879_RAT	Q5M879 rattus norv	674	226	5.7	437	1	TMPS4_HUMAN	Q9N854 homo sapien
602	231.5	5.9	624	2	Q2SMET7_RABIT	Q2SMET7 cryoclaugus	675	226	5.7	488	2	Q4RYB2_TETNG	Q4RYB2 tetraodon n
603	231.5	5.9	664	2	Q2MOM7_DROPS	Q2MOM7 drosophila	676	226	5.7	490	2	Q6PYD7_RAT	Q6PYD7 rattus norv
604	231.5	5.9	666	2	Q6VP08_DROVI	Q6VP08 drosophila	677	226	5.7	625	1	FALL_HUMAN	P03351 homo sapien
605	231.5	5.9	1157	2	Q17KM5_AEDAE	Q17KM5 aedes aegypt	678	226	5.7	625	2	Q4M5C2_ANOGA	Q4M5C2 homo sapien
606	231.5	5.9	242	2	Q93266_PSEAM	Q93266 pseudopleur	679	225.5	5.7	217	2	Q5THX3_HUMAN	Q5THX3 anopheles g
607	231	5.9	310	2	Q2YD02_BRARE	Q2YD02 brachydanio	680	225.5	5.7	312	2	Q7MT55_MOUSE	Q7MT55 mus musculu
608	231	5.9	338	2	Q16G08_AEDAE	Q16G08 aedes aegypt	681	225.5	5.7	347	1	HPT_PIG	Q88P87 sus scrofa
609	231	5.9	1008	1	TILL1_CHICK	Q9DET7 gallus gall	682	225.5	5.7	363	2	Q16XC4_AEDAE	Q16XC4 aedes aegypt
610	231	5.9	1012	1	TILL2_MOUSE	Q9WVW6 mus musculu	683	225.5	5.7	410	2	Q7Q956_ANOGA	Q7Q956 anopheles g
611	230.5	5.8	259	2	Q69E27_HUMAN	Q69E27 homo sapien	684	225.5	5.7	418	2	Q9VA87_DROME	Q9VA87 drosophila
612	230.5	5.8	295	2	Q69E28_HUMAN	Q69E28 homo sapien	685	225.5	5.7	429	2	Q8SZK2_DROME	Q8SZK2 drosophila
613	230	5.8	244	2	Q8QGV3_ANGUA	Q8QGV3 anguilla ja	686	225.5	5.7	418	2	Q8AVB0_BRARE	Q8AVB0 brachydanio
614	230	5.8	265	2	Q9VVT3_DROME	Q9VVT3 drosophila	687	225.5	5.7	457	1	TMPS5_HUMAN	Q9N883 homo sapien
615	230	5.8	318	2	Q7RTY9_HUMAN	Q7RTY9 homo sapien	688	225.5	5.7	1404	2	Q160R6_AEDAE	Q160R6 aedes aegypt

689	225	5.7	234	2	Q4RH74_TETNG	Q4rh74 tetradon n	762	221.5	5.6	247	2	Q547S4_BOVIN	Q547s4 bos taurus
690	225	5.7	237	2	Q7O0S6_ANOGA	Q7q0s6 anophelies g	763	221.5	5.6	271	2	Q803Z4_BRARE	Q803z4 brachydanio
691	225	5.7	328	2	Q8OZ40_RAT	Q8oz40 rattus norv	764	221.5	5.6	648	2	Q17MA3_AEDE	Q17ma3 aedes aegypt
692	225	5.7	347	1	HPT_PAPHA	Q5vanti papio hamad	765	221.5	5.6	2531	1	NOTCI_RAT	Q07008 rattus norv
693	225	5.7	387	2	Q9XT57_CTEFE	Q9xy57 ctenocephal	766	221.5	5.6	3620	1	CUBN_CANPA	Q9u033 canis famli
694	225	5.7	393	2	Q6RX66_JDIFT	Q6rx66 armigeres s	767	221	5.6	231	1	TRY2_SALSA	Q93032 salmo salar
695	225	5.7	455	2	Q8CDRO_MOUSE	Q8cdro mus musculu	768	221	5.6	258	2	Q97J39_PHASE	Q97j39 phaodon coc
696	225	5.7	490	2	Q7TN04_MOUSE	Q7tn04 mus musculu	769	221	5.6	264	2	Q2MOD7_DROPS	Q2mod7 drosoophila
697	225	5.7	490	2	Q920K3_RAT	Q920k3 rattus norv	770	221	5.6	268	1	CLCR_RAT	P55091 rattus norv
698	225	5.7	615	1	PA12_HUMAN	P00748 homo sapien	771	221	5.6	273	1	TRYB1_RAT	P27455 rattus norv
699	224.5	5.7	246	2	O883O1_MOUSE	O883o1 mus musculu	772	221	5.6	273	2	Q6P6W8_RAT	Q6p6w8 rattus norv
700	224.5	5.7	251	2	O548S4_RAT	O548s4 rattus norv	773	221	5.6	314	2	Q6RUT2_MOUSE	Q6rut2 mus musculu
701	224.5	5.7	253	2	Q91Y82_MOUSE	Q91y82 mus musculu	774	221	5.6	425	2	Q4SCU6_TETNG	Q4scu6 tetradon n
702	224.5	5.7	271	1	ELA2A_RAT	P00774 rattus norv	775	221	5.6	810	2	O5R8X6_PONPY	O5r8x6 pongo pygma
703	224.5	5.7	347	1	HPT_MOUSE	O61664 mus musculu	776	221	5.6	974	2	P916S8_DROME	P916s8 drosoophila
704	224.5	5.7	347	2	O3UES3_MOUSE	O3ubas m bone marr	777	221	5.6	1198	2	O5YRW3_HUMAN	O5yrw3 homo sapien
705	224.5	5.7	580	2	Q29DB1_DROPS	Q29db1 drosoophila	778	221	5.6	1299	2	Q7P1Q7_ANOGA	Q7p1q7 anophelies g
706	224.5	5.7	1022	1	TLL1_BRARE	O57460 brachydanio	779	221	5.6	1347	2	Q7PNR7_ANOGA	Q7pnr7 anophelies g
707	224.5	5.7	1427	2	O8AV11_ONCKE	O8av11 mesocricetu	780	220.5	5.6	250	2	Q8CGR5_MOUSE	O8cgr5 mus musculu
708	224	5.7	222	2	O8VIB7_MESAU	O8vib7 mesocricetu	781	220.5	5.6	277	2	Q8OMW7_MOUSE	Q8omw7 mus musculu
709	224	5.7	242	2	O8AV11_ONCKE	O8av11 oncorhynch	782	220.5	5.6	288	2	Q7Q9W5_ANOGA	Q7q9w5 anophelies g
710	224	5.7	245	1	CTRB_BOVIN	P00767 bos taurus	783	220.5	5.6	360	2	O17489_ANOGA	O17489 anophelies g
711	224	5.7	248	2	O161Z6_PASCI	O161z6 boletenia vi	784	220.5	5.6	360	2	Q7E9V7_ANOGA	Q7e9v7 anophelies g
712	224	5.7	261	1	KUK2_HOISE	Q6h321 equus cabal	785	220.5	5.6	468	2	Q9U0G3_PACLE	Q9u0g3 pacifastacu
713	224	5.7	343	2	O5RB12_PONPY	O5rb12 pongo pygma	786	220.5	5.6	808	2	Q7YU36_DROME	Q7yu36 drosoophila
714	224	5.7	484	2	Q31I08_HYLSY	Q31i08 hylobates s	787	220.5	5.6	814	2	O5DVP8_ONCMY	O5dvp8 oncorhynch
715	224	5.7	490	1	TMPS2_MOUSE	O91i08 mus musculu	788	220.5	5.6	1004	2	Q4SRX0_TETNG	Q4srx0 tetradon n
716	224	5.7	1174	2	O9VYR4_DROME	O9vyr4 drosoophila	789	220.5	5.6	1067	2	TLD_DROME	P25723 drosoophila
717	224	5.7	2602	2	Q7PSV8_DROME	Q7p8v8 anophelies g	790	220	5.6	1237	2	Q52VZ4_PONLE	Q52vz4 pontastacus
718	223.5	5.7	234	2	Q9O244_ACTIR	Q9o244 acipenser t	791	220	5.6	260	2	Q9W7P9_PAROL	Q9w7p9 paratichthy
719	223.5	5.7	266	2	Q9W7Q0_PAROL	Q9w7q0 paratichthy	792	220	5.6	261	2	Q962G7_CULPI	Q962g7 culx pipie
720	223.5	5.7	348	1	HPTR_HUMAN	O555e8 pongo sapien	793	220	5.6	275	1	TRYB1_HUMAN	O6b031 homo sapien
721	223.5	5.7	417	2	O5R5E8_PONPY	O5r5e8 pongo pygma	794	220	5.6	275	2	O6B0S1_HUMAN	O6b0s1 homo sapien
722	223.5	5.7	427	2	Q299R1_DROPS	Q299r1 drosoophila	795	220	5.6	331	2	O8RIAG_MOUSE	O8rix1 mus musculu
723	223.5	5.7	809	2	Q19A29_PIG	Q19a29 sus scrofa	796	220	5.6	331	2	O8OX17_MOUSE	O8ox17 mus musculu
724	223.5	5.7	1242	1	JAG1A_BRARE	Q90y57 brachydanio	797	220	5.6	527	2	Q17B77_AEDE	P70059 xenopus lae
725	223.5	5.7	1629	2	Q9V513_DROME	Q9v513 drosoophila	798	219.5	5.6	244	1	TRY2_XENIA	Q16h41 aedes aegypt
726	223.5	5.7	1674	2	O8SYG5_DROME	O8syg5 drosoophila	799	219.5	5.6	248	2	Q7S2T1_XENIA	Q7s2t1 xenopus lae
727	223	5.7	201	2	O5XUG4_DREAU	O5xug4 oreochromis	800	219.5	5.6	255	2	O961Y0_GALME	O961y0 galleria me
728	223	5.7	238	2	O16PK7_AEDAE	Q16pk7 aedes aegypt	801	219.5	5.6	255	2	O6GNU2_XENIA	O6gnu2 xenopus lae
729	223	5.7	242	2	Q9W7Q7_PAROL	Q9w7q7 paratichthy	802	219.5	5.6	255	2	Q4QR60_XENIA	Q4qr60 xenopus lae
730	223	5.7	261	2	O56GM3_CULPI	Q56gm3 culx pipie	803	219.5	5.6	259	2	Q3ZB43_MOUSE	Q3zb43 mus musculu
731	223	5.7	264	2	Q28Z63_DROPS	Q28z63 drosoophila	804	219.5	5.6	271	1	ELA2A_MOUSE	P05208 mus musculu
732	223	5.7	274	2	Q7O299_ANOGA	Q7q299 anophelies g	805	219.5	5.6	347	1	HPT_MUSCR	Q28x41 mus caroli
733	223	5.7	454	1	TMPS3_HUMAN	P57727 homo sapien	806	219.5	5.6	353	2	Q28X41_DROPS	Q28x41 drosoophila
734	223	5.7	538	2	OSUSC7_HUMAN	Q5usac7 homo sapien	807	219.5	5.6	482	2	Q16U16_AEDE	Q16u16 aedes aegypt
735	222.5	5.6	411	2	Q9VUF0_DROME	Q9vuf0 drosoophila	808	219.5	5.6	570	2	Q16H41_AEDE	P04186 mus musculu
736	222.5	5.6	417	1	HEPS_HUMAN	P05981 homo sapien	809	219.5	5.6	761	1	CFAB_MOUSE	Q3ueg8 mus musculu
737	222.5	5.6	434	1	UROK_CHICK	P15120 gallus galli	810	219.5	5.6	761	2	Q3UEG8_MOUSE	Q3ueh0 mus musculu
738	222.5	5.6	455	1	TMPS5_MOUSE	Q9per04 mus musculu	811	219.5	5.6	1378	2	Q3UHB0_MOUSE	Q3uhb0 mus musculu
739	222.5	5.6	514	2	Q2PKD2_XENIA	Q2pkd2 xenopus lae	812	219.5	5.6	1378	2	Q68HV2_MOUSE	Q68hv2 mus musculu
740	222.5	5.6	757	2	O2Y2P1_GINCI	Q2y2p1 ginglymosto	813	219.5	5.6	1444	2	O6A0S1_MOUSE	O6a0s1 mus musculu
741	222.5	5.6	790	1	PIAM_PIG	P06867 sus scrofa	814	219	5.6	249	2	Q7QAM5_ANOGA	Q7qam5 anophelies g
742	222.5	5.6	954	2	Q75UQ6_ACHTE	Q75uq6 achaeanea	815	219	5.6	287	2	Q171W2_AEDE	Q171w2 aedes aegypt
743	222	5.6	203	2	O5XUG5_ORENI	O5xug5 oreochromis	816	219	5.6	306	2	Q16RR3_AEDE	Q16rr3 aedes aegypt
744	222	5.6	267	2	O9V942_DROME	O9v942 drosoophila	817	219	5.6	318	2	Q80UR4_MOUSE	Q80ur4 mus musculu
745	222	5.6	269	1	ELA2A_PIG	P08419 sus scrofa	818	219	5.6	343	1	PRSS8_HUMAN	O16551 homo sapien
746	222	5.6	273	2	O921N4_MOUSE	O921n4 mus musculu	819	219	5.6	365	2	O97J66_HOLDI	O97j66 holotrichia
747	222	5.6	275	1	TRYA1_HUMAN	P15157 homo sapien	820	218.5	5.5	355	2	Q16EL5_AEDE	Q16el5 aedes aegypt
748	222	5.6	275	1	TRYB2_HUMAN	P20231 homo sapien	821	218.5	5.5	374	2	O81862_DERVA	O81862 dermacentor
749	222	5.6	275	2	O86TWS_HUMAN	Q86tm8 homo sapien	822	218.5	5.5	375	2	O817W8_DERAN	O817w8 dermacentor
750	222	5.6	275	2	O6B0S2_HUMAN	O6b0s2 homo sapien	823	218.5	5.5	435	1	TMPS4_MOUSE	O8vcv5 mus musculu
751	222	5.6	275	2	Q7O6S1_ANOGA	Q7o6s1 anophelies g	824	218.5	5.5	435	2	O16YAS_AEDE	O16yas aedes aegypt
752	222	5.6	276	2	O86UAS_HUMAN	Q86uas homo sapien	825	218.5	5.5	787	2	Q6S1G0_NAURA	Q6s1g0 najia kaotuch
753	222	5.6	282	2	O6NZY1_HUMAN	Q6nzy1 homo sapien	826	218.5	5.5	1007	1	TLL1_XENIA	O8j128 xenopus lae
754	222	5.6	345	2	O16G07_AEDAE	Q16g07 aedes aegypt	827	218.5	5.5	1379	2	Q6T2S6_HUMAN	O6t2s6 homo sapien
755	222	5.6	363	2	Q7PXS3_ANOGA	Q7pxs3 anophelies g	828	218	5.5	242	2	Q7SX90_BRARE	O7sx90 brachydanio
756	222	5.6	419	2	Q4M5P3_HUMAN	Q4m5p3 homo sapien	829	218	5.5	252	2	O5M908_XENIR	O5m908 xenopus tro
757	222	5.6	423	1	TM1LB_HUMAN	O9u152 homo sapien	830	218	5.5	260	2	Q7Q064_ANOGA	Q7q064 anophelies g
758	222	5.6	569	2	Q4RLS7_AEDAE	Q4rls7 aedes aegypt	831	218	5.5	271	2	O54213_STROR	O54213 streptomyce
759	222	5.6	658	2	Q4RLS7_TETNG	Q4rls7 tetradon n	832	218	5.5	370	2	Q17B76_AEDE	Q17b76 aedes aegypt
760	222	5.6	696	2	Q17IR1_AEDAE	Q17ir1 aedes aegypt	833	217.5	5.5	243	2	Q7MA13_MEGPE	Q7ma13 megabombus
761	222	5.6	761	2	Q4ORE3_BRARE	Q4qres brachydanio	834	217.5	5.5	269	2	O6ISU5_HUMAN	O6isus5 homo sapien

835	217.5	5.5	376	2	Q17EY0_AEDAE	Q17EY0 aedes aegypti	908	214.5	5.4	1322	2	Q9NATO_ANOGA	Q9NATO anopheles g
836	217.5	5.5	431	2	Q1URP2_MOUSE	Q1URP2 mus musculus	909	214.5	5.4	1428	1	ATRN_MOUSE	Q9N60 mus musculus
837	217.5	5.5	3570	2	Q7O737_ANOGA	Q7O737 anopheles g	910	214	5.4	252	2	Q5QBGO_9D1PT	Q9Q90 culicoides
838	217	5.5	229	1	KLX2_CAVPO	P12333 cavia porce	911	214	5.4	262	2	Q5G3K5_PYGNE	Q5G3K5 pygma
839	217	5.5	268	1	CLCR_HUMAN	Q99895 homo sapien	912	214	5.4	262	2	Q5G3K6_TYRFR	Q5G3K6 tirachyptb
840	217	5.5	273	1	TRYBI_MOUSE	Q02844 mus musculus	913	214	5.4	262	2	Q5G3K7_PYGBI	Q5G3K7 pygathix b
841	217	5.5	275	2	Q96RZ6_HUMAN	Q96RZ6 homo sapien	914	214	5.4	275	2	Q6FHB8_HUMAN	Q6FHB8 homo sapien
842	217	5.5	280	2	Q6GLK1_XENLA	Q6GLK1 xenopus lae	915	214	5.4	342	1	PRSS8_FAT	Q9E887 rattus norv
843	217	5.5	597	2	Q35727_MOUSE	Q35727 mus musculus	916	214	5.4	342	1	Q6GSY8_FAT	Q9E987 rattus norv
844	217	5.5	603	1	FAI2_CAVPO	Q04962 cavia porce	917	214	5.4	578	2	Q1DQ05_AEDAE	Q1DQ05 aedes aegypti
845	217	5.5	2703	1	NOTCH_DROME	P07207 drosophila	918	214	5.4	697	2	Q16WJ0_AEDAE	Q16WJ0 aedes aegypti
846	216.5	5.5	235	2	Q6B4R4_BOVIN	Q6B4R4 bos taurus	919	214	5.4	881	2	Q16L19_AEDAE	Q16L19 aedes aegypti
847	216.5	5.5	277	2	Q96899_9MYRI	Q96899 scolopendra	920	214	5.4	1290	2	Q16SA2_AEDAE	Q16SA2 aedes aegypti
848	216.5	5.5	288	1	Q16GG3_AEDAE	Q16GG3 aedes aegypti	921	213.5	5.4	241	2	Q98TG3_PYTLE	Q98TG3 engraulis j
849	216.5	5.5	365	1	HPTP_PATYR	Q28801 pan troglod	922	213.5	5.4	248	2	Q9VQ98_DROME	Q9VQ98 drosophila
850	216.5	5.5	365	2	Q7PWE1_ANOGA	Q7PWE1 anopheles g	923	213.5	5.4	249	2	Q7QKSO_ANOGA	Q7QKSO anopheles g
851	216.5	5.5	1048	2	Q4SJ96_TETNG	Q4SJ96 tetraodon n	924	213.5	5.4	251	2	Q4V675_DROME	Q4V675 drosophila
852	216.5	5.5	2528	2	Q8AXP0_CYNPY	Q8AXP0 cynops pyr	925	213.5	5.4	270	2	Q53CG5_BRARE	Q53CG5 brachydanto
853	216.5	5.5	2616	1	NUDEL_DROME	P98159 drosophila	926	213.5	5.4	314	2	Q175S1_AEDAE	Q175S1 aedes aegypti
854	216	5.5	255	2	Q7TN10_MOUSE	Q7TN10 mus musculus	927	213.5	5.4	381	2	Q7PN97_ANOGA	Q7PN97 anopheles g
855	216	5.5	259	2	Q4KIC6_XENLA	Q4KIC6 xenopus lae	928	213.5	5.4	442	1	TM1E_MOUSE	Q58248 mus musculus
856	216	5.5	268	2	Q35TP2_MOUSE	Q35TP2 mus musculus	929	213.5	5.4	543	1	TMPSD_MOUSE	Q58405 mus musculus
857	216	5.5	269	2	Q9D7T9_MOUSE	Q9D7T9 mus musculus	930	213.5	5.4	704	2	Q28ZD1_DROPS	Q28ZD1 drosophila
858	216	5.5	269	2	Q9CQ52_MOUSE	Q9CQ52 m adult mal	931	213.5	5.4	2352	2	Q61240_HALRO	Q61240 halocynthia
859	216	5.5	355	2	Q7PEW0_ANOGA	Q7PEW0 anopheles g	932	213	5.4	211	2	Q4SB50_TETNG	Q4SB50 tetraodon n
860	216	5.5	376	2	Q5TU09_ANOGA	Q5TU09 anopheles g	933	213	5.4	355	2	Q9NFT1_ANOGA	Q9NFT1 anopheles g
861	216	5.5	1218	1	JAG1_MOUSE	Q9QX00 mus musculus	934	213	5.4	394	2	P91817_TACTR	P91817 tachypleus
862	216	5.5	1218	2	Q3UVN4_MOUSE	Q3UVN4 mus musculus	935	213	5.4	541	2	Q4SM14_TETNG	Q4SM14 tetraodon n
863	215.5	5.5	243	1	Q9TXD8_AGEAP	Q9TXD8 agelenopsis	936	213	5.4	615	2	Q81Z25_HUMAN	Q81Z25 homo sapien
864	215.5	5.5	247	1	Q5H728_MACMU	P06872 canis famli	937	213	5.4	1243	2	Q17K13_AEDAE	Q17K13 aedes aegypti
865	215.5	5.5	248	1	TRY3_CHICK	Q90629 gallus galli	938	213	5.4	1477	2	Q4H3A4_CIOIN	Q4H3A4 ciona intes
866	215.5	5.5	252	2	Q3B898_XENLA	Q3B898 xenopus lae	939	212.5	5.4	242	2	Q7P0B3_ANOGA	Q7P0B3 anopheles g
867	215.5	5.5	253	2	Q3B856_MOUSE	Q3B856 mus musculus	940	212.5	5.4	247	2	Q35Y19_HUMAN	Q35Y19 homo sapien
868	215.5	5.5	254	2	Q8CGR4_MOUSE	Q8CGR4 mus musculus	941	212.5	5.4	260	2	Q7RTY3_HUMAN	Q7RTY3 anopheles g
869	215.5	5.5	259	2	Q6GN82_XENLA	Q6GN82 xenopus lae	942	212.5	5.4	265	2	Q4VB04_XENLA	Q4VB04 xenopus lae
870	215.5	5.5	317	1	BSSP4_HUMAN	Q9GZM4 homo sapien	943	212.5	5.4	282	1	KLK11_HUMAN	KLK11 mus musculus
871	215.5	5.5	321	2	Q80Y38_MOUSE	Q80Y38 mus musculus	944	212.5	5.4	339	2	Q99144_MOUSE	Q99144 mus musculus
872	215.5	5.5	326	2	Q9D9M0_MOUSE	Q9D9M0 mus musculus	945	212.5	5.4	397	2	Q7PZ85_ANOGA	Q7PZ85 anopheles g
873	215.5	5.5	415	2	Q17HP3_AEDAE	Q17HP3 aedes aegypti	946	212.5	5.4	420	2	Q61E14_RAT	Q61E14 rattus norv
874	215.5	5.5	429	2	Q16PK4_AEDAE	Q16PK4 aedes aegypti	947	212.5	5.4	501	2	Q28YV6_DROPS	Q28YV6 drosophila
875	215.5	5.5	562	2	Q675X7_OIKDI	Q675X7 oikopleura	948	212.5	5.4	693	2	Q2SHS3_HACHC	Q2SHS3 habella che
876	215.5	5.5	740	2	Q5RE78_PONPY	Q5RE78 pongo pygma	949	212.5	5.4	778	2	Q9VS19_DROME	Q9VS19 drosophila
877	215.5	5.5	751	2	Q6MG74_RAT	Q6MG74 rattus norv	950	212.5	5.4	849	1	POIS2_MOUSE	POIS2 mus musculus
878	215	5.4	211	1	TRYX_GADMO	Q91041 gadus morhu	951	212	5.4	260	1	NREN_MOUSE	NREN mus musculus
879	215	5.4	256	2	Q25081_HYPLI	Q25081 hypodermia 1	952	212	5.4	274	2	Q6GNFO_XENLA	Q6GNFO xenopus lae
880	215	5.4	260	2	Q7O5K4_ANOGA	Q7O5K4 anopheles g	953	212	5.4	340	2	Q8BJV6_MOUSE	Q8BJV6 mus musculus
881	215	5.4	270	2	Q7PKX5_ANOGA	Q7PKX5 anopheles g	954	212	5.4	875	2	Q5DPTJ_MOUSE	Q5DPTJ mus musculus
882	215	5.4	388	2	Q4RRR7_TETNG	Q4RRR7 tetraodon n	955	212	5.4	1322	2	Q9NMJ5_ANOGA	Q9NMJ5 anopheles g
883	215	5.4	389	2	Q9PVX7_XENLA	Q9PVX7 xenopus lae	956	212	5.4	2031	2	Q29G88_DROPS	Q29G88 drosophila
884	215	5.4	422	2	Q4RG82_TETNG	Q4RG82 tetraodon n	957	211.5	5.4	257	2	Q16CM9_AEDAE	Q16CM9 aedes aegypti
885	215	5.4	597	2	Q6PER0_MOUSE	Q6PER0 mus musculus	958	211.5	5.4	272	2	Q7PWE5_ANOGA	Q7PWE5 anopheles g
886	215	5.4	609	2	Q8OYC5_MOUSE	Q8OYC5 mus musculus	959	211.5	5.4	402	2	Q2TBU0_BOVIN	Q2TBU0 bos taurus
887	215	5.4	749	2	Q9YGB8_ONCMY	Q9YGB8 oncorhynch	960	211.5	5.4	413	1	Q5M8B7_XENTR	Q5M8B7 xenopus tro
888	215	5.4	760	2	Q8JG08_TETNG	Q8JG08 tetraodon n	961	211.5	5.4	418	2	TM1LD_HUMAN	TM1LD homo sapien
889	215	5.4	762	2	Q4SFT0_TETNG	Q4SFT0 tetraodon n	962	211.5	5.4	484	2	Q7QCV0_ANOGA	Q7QCV0 anopheles g
890	215	5.4	810	1	PLMN_HUMAN	P00747 homo sapien	963	211.5	5.4	629	2	Q6AZS7_XENLA	Q6AZS7 xenopus lae
891	215	5.4	810	2	Q5TER4_HUMAN	Q5TER4 homo sapien	964	211.5	5.4	719	2	Q6DJ90_XENTR	Q6DJ90 xenopus tro
892	215	5.4	1116	2	Q7TP05_RAT	Q7TP05 rattus norv	965	211	5.3	237	1	Q29464_BOVIN	Q29464 bos taurus
893	215	5.4	1497	2	Q5T938_HUMAN	Q5T938 homo sapien	966	211	5.3	276	1	MCPT6_MOUSE	MCPT6 mus musculus
894	215	5.4	215	2	Q819P3_AURAU	Q819P3 aurelia aur	967	211	5.3	313	2	Q7PFX3_ANOGA	Q7PFX3 anopheles g
895	214.5	5.4	195	2	Q5BEB2_XENTR	Q5BEB2 xenopus tro	968	211	5.3	444	2	Q170T8_AEDAE	Q170T8 aedes aegypti
896	214.5	5.4	244	1	Q5BEB2_XENTR	Q5BEB2 xenopus tro	969	211	5.3	510	2	Q7Q554_ANOGA	Q7Q554 anopheles g
897	214.5	5.4	247	1	TRY2_BOVIN	Q29463 bos taurus	970	211	5.3	650	2	Q17MA7_AEDAE	Q17MA7 aedes aegypti
898	214.5	5.4	249	2	Q6DIW2_XENTR	Q6DIW2 xenopus tro	971	211	5.3	1218	1	JAG1_HUMAN	JAG1 homo sapien
899	214.5	5.4	273	1	TRY1_ANOGA	P35035 bombyx mori	972	211	5.3	1218	2	Q4KMR2_HUMAN	Q4KMR2 homo sapien
900	214.5	5.4	366	2	Q45RG0_BOMMO	Q45RG0 bombyx mori	973	211	5.3	2447	2	Q13149_FUGRU	Q13149 fuigu
901	214.5	5.4	505	2	Q966V4_HALRO	Q966V4 halocynthia	974	210.5	5.3	247	1	TRYP_STMYI	TRYP simulium vl
902	214.5	5.4	570	2	Q172N8_AEDAE	Q172N8 aedes aegypti	975	210.5	5.3	275	1	TRY3_ANOGA	TRY3 anopheles g
903	214.5	5.4	593	2	Q172N8_AEDAE	Q172N8 aedes aegypti	976	210.5	5.3	280	2	Q8N171_HUMAN	Q8N171 homo sapien
904	214.5	5.4	593	1	FAI2_BOVIN	P98140 bos taurus	977	210.5	5.3	300	2	Q5W8S2_MOUSE	Q5W8S2 mus musculus
905	214.5	5.4	1019	2	Q16XC0_AEDAE	Q16XC0 aedes aegypti	978	210.5	5.3	342	1	PRSS8_MOUSE	PRSS8 mus musculus
906	214.5	5.4	1130	2	Q7QIM7_ANOGA	Q7QIM7 anopheles g	979	210.5	5.3	360	2	Q9W1X6_DROME	Q9W1X6 drosophila
907	214.5	5.4	1309	2	Q16TMD_AEDAE	Q16TMD aedes aegypti	980	210.5	5.3	470	2	Q173L6_AEDAE	Q173L6 aedes aegypti

981	210.5	5.3	572	1	TMPS1_HUMAN	Q7FY8	homo sapien	1054	206.5	5.2	321	1	TRYG1_HUMAN	Q8H12	homo sapien
982	210.5	5.3	572	2	Q17R4_HUMAN	Q17H4	homo sapien	1055	206.5	5.2	359	2	Q7Q56_ANOGA	Q7Q56	ANOGA
983	210.5	5.3	572	2	Q28290_CANFA	Q28290	canis famli	1056	206.5	5.2	467	2	Q86W2_HUMAN	Q86W2	HUMAN
984	210.5	5.3	855	1	POL52_HUMAN	Q5K43	homo sapien	1057	206.5	5.2	476	2	Q5T59_HUMAN	Q5T59	HUMAN
985	210.5	5.3	1219	1	JAG1_RAT	Q63722	rattus norv	1058	206.5	5.2	573	2	Q5V516_DROME	Q5V516	DROME
986	210	5.3	262	2	Q5Kf6_BUNHO	Q5Kf6	bonithecu	1059	206.5	5.2	728	2	Q7Q8B4_ANOGA	Q7Q8B4	ANOGA
987	210	5.3	750	1	CO2_BOVIN	Q3Y42	bos taurus	1060	206.5	5.2	741	2	Q4S1U3_TETNG	Q4S1U3	TETNG
988	210	5.3	2437	1	NOTC1_BRARE	P46530	brachydanto	1061	206.5	5.2	837	2	Q1M557_RHIL3	Q1M557	RHIL3
989	209.5	5.3	260	2	Q3KQ12_XENLA	Q3KQ12	xenopus lae	1062	206.5	5.2	1065	2	Q810H2_MOUSE	Q810H2	MOUSE
990	209.5	5.3	280	1	TRYM_CANFA	P19236	canis famli	1063	206.5	5.2	1403	2	Q7Q820_MOUSE	Q7Q820	MOUSE
991	209.5	5.3	313	2	OBIN51_DROME	Q6N51	drosophila	1064	206	5.2	238	2	Q7QK8_ANOGA	Q7QK8	ANOGA
992	209.5	5.3	347	1	HPT_MUSSA	Q6N558	mus saxicol	1065	206	5.2	263	2	Q9N892_AGRIP	Q9N892	AGRIP
993	209.5	5.3	423	2	Q5FBE1_HUMAN	Q5FBE1	homo sapien	1066	206	5.2	264	2	Q4RZ78_TETNG	Q4RZ78	TETNG
994	209.5	5.3	441	2	Q17Q79_AEDAE	Q17Q79	aedes aegypt	1067	206	5.2	269	2	Q6AZ79_XENLA	Q6AZ79	XENLA
995	209.5	5.3	516	2	Q17BQ4_AEDAE	Q17BQ4	aedes aegypt	1068	206	5.2	374	2	Q49QW1_SPOLT	Q49QW1	SPOLT
996	209.5	5.3	562	2	Q1RMF8_HUMAN	Q1RMF8	homo sapien	1069	206	5.2	389	2	Q3UQ41_MOUSE	Q3UQ41	MOUSE
997	209.5	5.3	875	1	POL52_RAT	Q5K297	rattus norv	1070	206	5.2	395	2	Q6R559_OSTNU	Q6R559	OSTNU
998	209.5	5.3	1441	2	Q723G3_HUMAN	Q723G3	homo sapien	1071	206	5.2	429	2	Q17319_AEDAE	Q17319	AEDAE
999	209.5	5.3	1492	2	Q29F55_DROPS	Q29F55	drosophila	1072	206	5.2	492	2	Q7Z155_9EUC4	Q7Z155	9EUC4
1000	209	5.3	263	1	AMI_XENLA	Q632K0	xenopus lae	1073	206	5.2	826	2	Q1Q6B1_AEDAE	Q1Q6B1	AEDAE
1001	209	5.3	279	2	Q4RG3_TETNG	Q4RG3	tetradon n	1074	206	5.2	1161	2	Q16WU3_AEDAE	Q16WU3	AEDAE
1002	209	5.3	340	2	Q21624_GLOMR	Q21624	glossina mo	1075	206	5.2	2040	2	Q5VTD7_HUMAN	Q5VTD7	HUMAN
1003	209	5.3	384	2	Q9W630_CYPCA	Q9W630	cyrtinus ca	1076	206	5.2	2040	2	Q1HP67_HUMAN	Q1HP67	HUMAN
1004	209	5.3	401	2	Q7QKD2_ANOGA	Q7QKD2	anopheles g	1077	206	5.2	4548	2	APCA_HUMAN	APCA	HUMAN
1005	209	5.3	433	1	UROK_MOUSE	P06869	m urokinase	1078	205.5	5.2	245	2	Q7PQ89_ANOGA	Q7PQ89	ANOGA
1006	209	5.3	893	2	Q613J2_CABBR	Q613J2	caenorhabdi	1079	205.5	5.2	257	2	Q5QB15_9DIPT	Q5QB15	9DIPT
1007	208.5	5.3	236	2	Q9TYH3_SCMA	Q9TYH3	schistosoma	1080	205.5	5.2	269	2	Q6IS45_HUMAN	Q6IS45	HUMAN
1008	208.5	5.3	258	2	Q28803_PANTR	Q28803	pan troglod	1081	205.5	5.2	269	2	Q6ISP9_HUMAN	Q6ISP9	HUMAN
1009	208.5	5.3	311	2	Q80X23_RAT	Q80X23	rattus norv	1082	205.5	5.2	284	2	Q16Y22_AEDAE	Q16Y22	AEDAE
1010	208.5	5.3	322	2	Q16FK7_AEDAE	Q16FK7	aedes aegypt	1083	205.5	5.2	347	1	HPT_RAT	HPT_RAT	
1011	208.5	5.3	371	2	Q17FW3_AEDAE	Q17FW3	aedes aegypt	1084	205.5	5.2	357	2	Q5MPE8_MANSE	Q5MPE8	MANSE
1012	208.5	5.3	417	1	TM1D_MOUSE	Q8VhK8	m transemb	1085	205.5	5.2	363	2	Q2VPP0_XENLA	Q2VPP0	XENLA
1013	208.5	5.3	444	2	Q9V4W6_DROME	Q9V4W6	drosophila	1086	205.5	5.2	374	2	Q8OY05_MOUSE	Q8OY05	MOUSE
1014	208.5	5.3	464	2	Q6L7Z5_HAELO	Q6L7Z5	haemaphysal	1087	205.5	5.2	416	2	Q8B213_MOUSE	Q8B213	MOUSE
1015	208.5	5.3	581	1	TMPS2_HUMAN	Q9Y92	homo sapien	1088	205.5	5.2	416	2	Q8B230_MOUSE	Q8B230	MOUSE
1016	208	5.3	256	2	Q25082_HYPLI	Q25082	hypoderma l	1089	205.5	5.2	470	2	Q5CZL0_XENTR	Q5CZL0	XENTR
1017	208	5.3	271	2	Q8HYJ2_BOVIN	Q8HYJ2	bos taurus	1090	205.5	5.2	492	1	TMPS2_HUMAN	TMPS2	HUMAN
1018	208	5.3	275	2	Q8IXD7_HUMAN	Q8IXD7	homo sapien	1091	205.5	5.2	492	2	Q6GTG7_HUMAN	Q6GTG7	HUMAN
1019	208	5.3	295	2	Q7Q6S2_ANOGA	Q7Q6S2	anopheles g	1092	205.5	5.2	752	2	Q5R8B4_PONPY	Q5R8B4	PONPY
1020	208	5.3	326	2	Q7RTY6_HUMAN	Q7RTY6	homo sapien	1093	205.5	5.2	840	2	Q2KOC3_RHIEC	Q2KOC3	RHIEC
1021	208	5.3	352	2	Q16H66_AEDAE	Q16H66	aedes aegypt	1094	205	5.2	220	2	Q4L1L4_9NEOP	Q4L1L4	9NEOP
1022	208	5.3	357	2	Q4KLE1_XENLA	Q4LE1	xenopus lae	1095	205	5.2	256	1	HYPB_HYPLI	HYPB	HYPLI
1023	208	5.3	525	2	Q17GJ5_AEDAE	Q17GJ5	aedes aegypt	1096	205	5.2	264	2	Q0Z5F9_CULOU	Q0Z5F9	CULOU
1024	208	5.3	534	2	Q176U7_AEDAE	Q176U7	aedes aegypt	1097	205	5.2	273	2	Q16KW4_AEDAE	Q16KW4	AEDAE
1025	207.5	5.3	195	2	Q8J006_HUMAN	Q8J006	homo sapien	1098	205	5.2	346	2	Q4EY35_TETNG	Q4EY35	TETNG
1026	207.5	5.3	239	2	Q91218_ONCMY	Q91218	oncorhynch	1099	205	5.2	445	2	Q16UV5_AEDAE	Q16UV5	AEDAE
1027	207.5	5.3	247	2	Q17LZ9_AEDAE	Q17LZ9	aedes aegypt	1100	205	5.2	492	2	Q96T73_HUMAN	Q96T73	HUMAN
1028	207.5	5.3	256	1	TRYB_MANSE	P35046	manduca sex	1101	205	5.2	870	2	Q81Q66_DROME	Q81Q66	DROME
1029	207.5	5.3	266	2	Q92077_GADMO	Q92077	gadus moru	1102	205	5.2	4181	2	Q291E2_DROPS	Q291E2	DROPS
1030	207.5	5.3	269	1	ELAZA_HUMAN	P08217	homo sapien	1103	204.5	5.2	246	1	TRY2_RAT	TRY2	RAT
1031	207.5	5.3	269	2	Q6ISN8_HUMAN	Q6ISN8	homo sapien	1104	204.5	5.2	247	2	Q9CPN9_MOUSE	Q9CPN9	MOUSE
1032	207.5	5.3	298	2	Q9NH06_HELZE	Q9NH06	heliothis z	1105	204.5	5.2	247	2	Q9D7V7_MOUSE	Q9D7V7	MOUSE
1033	207.5	5.3	778	2	Q28D44_XENTR	Q28D44	xenopus tro	1106	204.5	5.2	256	1	TRYC_MANSE	TRYC	MANSE
1034	207.5	5.3	900	2	Q6AK42_XENLA	Q6AK42	xenopus lae	1107	204.5	5.2	281	2	Q46137_LUMRU	Q46137	LUMRU
1035	207.5	5.3	1010	2	Q4SQ11_TETNG	Q4SQ11	tetradon n	1108	204.5	5.2	311	2	Q4V3F4_DROME	Q4V3F4	DROME
1036	207.5	5.3	1282	2	Q8TER0_HUMAN	Q8TER0	homo sapien	1109	204.5	5.2	367	2	Q4V3K5_DROSOPH	Q4V3K5	DROSOPH
1037	207	5.2	225	2	Q5TAH7_HUMAN	Q5TAH7	homo sapien	1110	204.5	5.2	367	2	Q7O169_MOUSE	Q7O169	MOUSE
1038	207	5.2	238	1	TRY5_AEDAE	P23787	aedes aegypt	1111	204.5	5.2	373	2	Q4V3X9_DROME	Q4V3X9	DROME
1039	207	5.2	240	2	Q7SY06_XENLA	Q7SY06	xenopus lae	1112	204.5	5.2	449	2	Q95RA3_DROME	Q95RA3	DROME
1040	207	5.2	260	1	NRPN_RAT	Q86780	rattus norv	1113	204.5	5.2	470	2	Q661F4_XENTR	Q661F4	XENTR
1041	207	5.2	266	2	Q161D7_AEDAE	Q161D7	aedes aegypt	1114	204.5	5.2	752	1	CO2_PONPY	CO2	PONPY
1042	207	5.2	274	2	Q7Q2X2_ANOGA	Q7Q2X2	anopheles g	1115	204.5	5.2	768	2	Q5T146_HUMAN	Q5T146	HUMAN
1043	207	5.2	426	2	Q5T6B5_HUMAN	Q5T6B5	homo sapien	1116	204.5	5.2	1008	2	Q336F5_HUMAN	Q336F5	HUMAN
1044	207	5.2	1957	2	Q4SIU8_TETNG	Q4SIU8	homo sapien	1117	204.5	5.2	1497	2	Q8NBN9_HUMAN	Q8NBN9	HUMAN
1045	206.5	5.2	195	2	Q6SPC0_HUMAN	Q6SPC0	homo sapien	1118	204.5	5.2	2470	1	NOTC2_MOUSE	NOTC2	MOUSE
1046	206.5	5.2	247	2	Q17W1_AEDAE	Q17W1	aedes aegypt	1119	204.5	5.2	2483	2	Q29DR0_DROPS	Q29DR0	DROPS
1047	206.5	5.2	256	2	TRYA_MANSE	P35045	manduca sex	1120	204	5.2	190	2	Q5T7B8_ANOGA	Q5T7B8	ANOGA
1048	206.5	5.2	269	2	Q6ICV2_HUMAN	Q6ICV2	homo sapien	1121	204	5.2	220	2	Q4L1L5_9NEOP	Q4L1L5	9NEOP
1049	206.5	5.2	269	2	Q96QV5_HUMAN	Q96QV5	homo sapien	1122	204	5.2	248	2	Q16PR8_AEDAE	Q16PR8	AEDAE
1050	206.5	5.2	269	2	Q9V929_DROME	Q9V929	homo sapien	1123	204	5.2	260	1	NRPN_HUMAN	NRPN	HUMAN
1051	206.5	5.2	270	2	Q27824_UCAPU	Q27824	uca pugilac	1124	204	5.2	266	2	Q17FW5_AEDAE	Q17FW5	AEDAE
1052	206.5	5.2	274	2	Q7Q092_ANOGA	Q7Q092	anopheles g	1125	204	5.2	395	2	Q8W58_OSTNU	Q8W58	OSTNU
1053	206.5	5.2	284	2	Q8NF86_HUMAN	Q8NF86	homo sapien	1126	204	5.2	417	1	TM1D_RAT	TM1D	RAT
9812						homo sapien									
97526						anopheles g									
Q86W2						homo sapien									
Q5T59						homo sapien									
Q9V516						drosophila									
Q7QBP4						anopheles g									
Q4S1U3						tetng									
Q1M557						rhizodum l									
Q810H2						mus muscullu									
Q7Q820						mus muscullu									
Q7QK8						anopheles g									
Q9N892						agrotis ips									
Q4Z78						tetradon n									
Q6AZ79						xenopus lae									
Q49QW1						spodoptera									
Q3UQ41						mus muscullu									
Q6R559						ostria nu									
Q17319						aedes aegypt									
Q7Z155						chitromates									
Q16QB1						aedes aegypt									
Q16WU3						aedes aegypt									
Q5VTD7						homo sapien									
Q1															

1127	204	5.2	645	2	OSRG6 BRARE	OSrg6 brachydanio	1200	201	5.1	484	2	Q311V5 PANTR	Q311V5 pan troglod
1128	203.5	5.2	195	2	Q81XB4_HUMAN	Q81xb4 homo sapien	1201	201	5.1	490	2	Q52KX2_MOUSE	Q52kx2 mus musculus
1129	203.5	5.2	238	2	Q70P40_ANOGA	Q70f40 anophelies g	1202	201	5.1	493	2	Q17064_AEDAE	Q17064 aedes aegypt
1130	203.5	5.2	247	1	TR12_HUMAN	P07478 homo sapien	1203	201	5.1	591	2	Q176D9_AEDAE	Q176d9 aedes aegypt
1131	203.5	5.2	247	2	Q35Y20_HUMAN	Q35y20 homo sapien	1204	201	5.1	145	2	Q5SPB5_BRARE	Q5spb5 brachydanio
1132	203.5	5.2	247	2	Q5NV50_HUMAN	Q5nv56 homo sapien	1205	200.5	5.1	668	2	Q5J326_ORMEO	Q5j326 oreochromis
1133	203.5	5.2	261	2	Q725F3_HUMAN	Q725f3 homo sapien	1206	200.5	5.1	231	1	TR9Y_PIG	P00761 sus scrofa
1134	203.5	5.2	263	1	CPAD_RAT	P32038 rattus norv	1207	200.5	5.1	246	2	Q792Z1_MOUSE	Q792z1 mus musculus
1135	203.5	5.2	285	1	FA9_CAVRO	P16295 cavia porce	1208	200.5	5.1	247	2	Q5H729_MACMU	Q5h729 macaca mula
1136	203.5	5.2	294	2	Q3V068_MOUSE	Q3V068 mus musculus	1209	200.5	5.1	249	2	Q9W7Q1_PAPOL	Q9w7q1 papallithy
1137	203.5	5.2	309	2	Q27083_TACTR	Q27083 tachyples	1210	200.5	5.1	260	2	Q17J19_AEDAE	Q17j19 aedes aegypt
1138	203.5	5.2	335	2	Q8V1F2_MOUSE	Q8v1f2 mus musculus	1211	200.5	5.1	281	2	Q6N8B4_HUMAN	Q6n8b4 homo sapien
1139	203.5	5.2	420	2	Q16076_AEDAE	Q16076 aedes aegypt	1212	200.5	5.1	288	2	Q16JMT2_HUMAN	Q16jmt2 aedes aegypt
1140	203.5	5.2	664	1	DLIC_BRARE	Q91ac6 brachydanio	1213	200.5	5.1	351	2	Q17763_AEDAE	Q17763 aedes aegypt
1141	203.5	5.2	734	2	Q69D12_PIG	Q69d12 sus scrofa	1214	200.5	5.1	358	2	Q57434_FUGRU	Q57434 fugu rubrip
1142	203.5	5.2	750	2	Q9W633_CYPCA	Q9w633 cyprinus ca	1215	200.5	5.1	372	2	Q16PM8_AEDAE	Q16pm8 aedes aegypt
1143	203.5	5.2	1323	2	Q72387_HUMAN	Q72387 homo sapien	1216	200.5	5.1	415	1	PCOC2_HUMAN	Q9uk29 homo sapien
1144	203.5	5.2	1432	1	ATRN_RAT	Q9186 rattus norv	1217	200.5	5.1	583	2	Q16K16_AEDAE	Q16k16 aedes aegypt
1145	203.5	5.2	2067	2	Q59ED8_HUMAN	Q59ed8 homo sapien	1218	200.5	5.1	752	1	CO2_HUMAN	Q53hp3 homo sapien
1146	203.5	5.2	2555	2	Q55XM3_HUMAN	Q55xm3 homo sapien	1219	200.5	5.1	752	2	Q53HP3_HUMAN	Q53hp3 homo sapien
1147	203.5	5.2	3398	2	Q29P22_DROPS	Q29p22 dtrosophila	1220	200.5	5.1	752	2	Q5JP69_HUMAN	Q5jp69 homo sapien
1148	203.5	5.2	3494	2	Q7LCS3_HUMAN	Q7lcs3 homo sapien	1221	200.5	5.1	810	1	PLMN_MACMU	P12545 macaca mula
1149	203	5.1	254	2	Q5M8G2_XENTR	Q5m8g2 xenopus tro	1222	200.5	5.1	951	1	NAS39_CAEEL	Q20176 caenorhabd
1150	203	5.1	255	2	Q70HS0_ANOGA	Q70hs0 anophelies g	1223	200	5.1	247	2	Q42158_PETMA	Q42158 petromyzon
1151	203	5.1	266	2	Q16TMI_AEDAE	Q16tmi aedes aegypt	1224	200	5.1	358	2	Q171W3_AEDAE	Q171w3 aedes aegypt
1152	203	5.1	370	2	Q9VAA4_DROME	Q9vaa4 dtrosophila	1225	200	5.1	385	1	TSP50_HUMAN	Q9u138 homo sapien
1153	203	5.1	403	2	Q9KS06_VIBCH	Q9ks06 vibrio chol	1226	200	5.1	454	2	Q46506_PAPHA	Q46506 papio hamad
1154	203	5.1	520	2	Q21622_GLOMR	Q21622 glostina mo	1227	200	5.1	504	2	Q9VEM0_DROME	Q9vem0 dtrosophila
1155	203	5.1	680	2	Q1L8K4_BRARE	Q1l8k4 brachydanio	1228	200	5.1	564	2	Q7RTZ1_HUMAN	Q7rtz1 homo sapien
1156	203	5.1	833	2	Q9Y1C5_CYPCA	Q9y1c5 cyprinus ca	1229	200	5.1	2061	2	Q4SRM9_TETNG	Q4srn9 tetraodon n
1157	202.5	5.1	239	2	Q8N1C9_HUMAN	Q8n1c9 homo sapien	1230	200	5.1	3564	2	Q16KG3_AEDAE	Q16kg3 aedes aegypt
1158	202.5	5.1	255	1	KLK15_SNGOE	Q7j166 saguinus oe	1231	199.5	5.1	223	2	Q9VAY4_DROME	Q9vay4 dtrosophila
1159	202.5	5.1	274	2	Q16133_ANOST	Q16133 anophelies s	1232	199.5	5.1	243	2	Q5M902_XENTR	Q5m902 xenopus tiro
1160	202.5	5.1	339	2	Q6BDA8_PENUP	Q6bd88 penaeus jap	1233	199.5	5.1	247	1	TR9Y_RAT	P08426 rattus norv
1161	202.5	5.1	347	2	Q5EBB4_RAT	Q5ebd4 rattus norv	1234	199.5	5.1	257	1	Q5X1Z0_BRARE	Q5x1z0 brachydanio
1162	202.5	5.1	372	2	Q9W2C8_DROME	Q9w2c8 dtrosophila	1235	199.5	5.1	257	1	KLK1_MACFA	Q07726 macaca fasc
1163	202.5	5.1	431	2	Q16PK6_AEDAE	Q16pk6 aedes aegypt	1236	199.5	5.1	258	2	Q5VANA_CERTO	Q5vna4 cercocobus
1164	202.5	5.1	1327	2	Q59ED1_HUMAN	Q59ed1 homo sapien	1237	199.5	5.1	258	2	Q28508_MACMU	Q28508 macaca mula
1165	202.5	5.1	3623	1	CUBN_HUMAN	P60494 gadus morhu	1238	199.5	5.1	348	2	Q86W55_HUMAN	Q86w55 homo sapien
1166	202.5	5.1	241	1	TR9Y_GADMO	P00752 sus scrofa	1239	199.5	5.1	378	2	Q90WP0_TRASC	Q90wp0 tracheams s
1167	202	5.1	246	2	KLK_PIG	Q7q9x5 anophelies g	1240	199.5	5.1	405	2	Q1ZEY4_GGAMM	Q1zey4 psychromona
1168	202	5.1	249	2	Q7Q9X5_ANOGA	Q7q9x5 aedes aegypt	1241	199.5	5.1	1193	2	Q90819_CHICK	Q90819 gallus gall
1169	202	5.1	263	2	Q4L1K1_9NEOP	Q4l1k1 sesamia non	1242	199.5	5.1	2565	1	NOTC1_HUMAN	P46531 homo sapien
1170	202	5.1	312	2	Q16ZB8_AEDAE	Q16z88 aedes aegypt	1243	199.5	5.1	2633	2	Q25253_LUCCU	Q25253 lucilia cup
1171	202	5.1	331	2	Q32N63_XENIA	Q32n63 xenopus lae	1244	199.5	5.1	264	2	Q5XG53_XENIA	Q5xg53 xenopus lae
1172	202	5.1	380	2	Q68D21_HUMAN	Q68d21 homo sapien	1245	199	5.0	254	2	Q5T552_ANOGA	Q5t552 anophelies g
1173	202	5.1	394	2	Q5MPB7_MANSE	Q5mpb7 manduca sex	1246	199	5.0	191	2	Q5XG53_XENIA	Q5xg53 xenopus lae
1174	202	5.1	488	2	Q81UV8_HUMAN	Q81uv8 homo sapien	1247	199	5.0	260	2	Q16TMO_AEDAE	Q16tmo aedes aegypt
1175	202	5.1	605	2	Q5MPB8_MANSE	Q5mpb8 manduca sex	1248	199	5.0	263	2	Q62562_PENVA	Q62562 penaeus lae
1176	202	5.1	743	2	Q9YGE7_ONCMY	Q9yge7 oncothychnu	1249	199	5.0	264	2	Q6GPy5_XENIA	Q6gpy5 xenopus lae
1177	202	5.1	797	2	Q501G6_ORYILA	Q501g6 oryzias lat	1250	199	5.0	264	2	Q8QGf6_XENIA	Q8qgf6 xenopus lae
1178	202	5.1	2321	1	NOTC3_HUMAN	Q9um47 homo sapien	1251	199	5.0	266	2	Q5MBV7_XENTR	Q5mbv7 xenopus tro
1179	201.5	5.1	195	2	Q8J007_HUMAN	Q8j007 homo sapien	1252	199	5.0	268	2	Q51829_MAYDE	Q51829 mayetolia d
1180	201.5	5.1	195	2	Q8J008_HUMAN	Q8j008 homo sapien	1253	199	5.0	317	2	Q3JMG7_MOUSE	Q3jmg7 mus musculus
1181	201.5	5.1	246	1	TR9Y_MOUSE	P07146 mus musculus	1254	199	5.0	355	2	Q176U9_AEDAE	Q176u9 aedes aegypt
1182	201.5	5.1	246	2	Q792T6_MOUSE	Q792t6 mus musculus	1255	199	5.0	401	2	Q6LH17_PHOBR	Q6lh17 photobacter
1183	201.5	5.1	255	2	Q61S10_HUMAN	Q61s10 homo sapien	1256	199	5.0	441	2	Q9XXV0_BOMMO	Q9xxv0 bombyx mori
1184	201.5	5.1	256	1	KLK15_HUMAN	Q9hzus xenopus tro	1257	199	5.0	683	3	Q1ECY3_BRARE	Q1ecy3 brachydanio
1185	201.5	5.1	265	2	Q5HZU5_XENTR	Q5hzus xenopus tro	1258	198.5	5.0	1303	2	Q66S84_OIKDI	Q66s84 oikopleura
1186	201.5	5.1	293	2	Q16ZET_AEDAE	Q16zet aedes aegypt	1259	198.5	5.0	237	2	Q17035_ANOGA	Q17035 anophelies g
1187	201.5	5.1	320	2	Q7TOX2_XENIA	Q7tox2 xenopus lae	1260	198.5	5.0	243	1	TR9Y_BOVIN	P00760 bos taurus
1188	201.5	5.1	344	2	Q640F8_XENIA	Q640f8 xenopus lae	1261	198.5	5.0	260	2	Q7S2C3_CHICK	Q7s2c3 gallus gall
1189	201.5	5.1	383	2	Q7PQ76_ANOGA	Q7pq76 anophelies g	1262	198.5	5.0	311	1	TR9Y1_MOUSE	Q9u173 mus musculus
1190	201.5	5.1	415	2	Q53EK6_HUMAN	Q53ek6 homo sapien	1263	198.5	5.0	357	2	Q7PVQ3_ANOGA	Q7pvq3 anophelies g
1191	201.5	5.1	438	2	Q6ZWK6_HUMAN	Q6zwk6 homo sapien	1264	198.5	5.0	364	2	Q7O1D1_ANOGA	Q7o1d1 anophelies g
1192	201.5	5.1	597	2	Q4SMT3_TETNG	Q4smt3 tetraodon n	1265	198.5	5.0	364	2	Q9NAS9_ANOGA	Q9nas9 anophelies g
1193	201	5.1	247	2	Q42608_PETMA	Q42608 petromyzon	1266	198.5	5.0	373	2	Q16GX3_AEDAE	Q16gx3 aedes aegypt
1194	201	5.1	248	2	Q66L05_XENIA	Q66l05 xenopus lae	1267	198.5	5.0	382	2	Q179E4_AEDAE	Q179e4 aedes aegypt
1195	201	5.1	260	2	Q81W69_HUMAN	Q81w69 homo sapien	1268	198.5	5.0	388	2	Q44330_MANSE	Q44330 manduca sex
1196	201	5.1	275	2	Q66UD0_9DIPR	Q66ud0 culicoides	1269	198.5	5.0	461	2	Q874N2_RH1AP	Q874n2 rhinicephal
1197	201	5.1	351	2	Q816K0_HOLDI	Q816k0 holotrichia	1270	198.5	5.0	752	1	CO2_GORGO	Q863ao gorilla gor
1198	201	5.1	392	2	Q9VMZ3_DROME	Q9vmz3 dtrosophila	1271	198.5	5.0	829	2	Q5TF49_HUMAN	Q5tf49 homo sapien
1199	201	5.1	484	2	Q311V4_PANPA	Q311v4 pan paniscu	1272	198.5	5.0	829	2	Q4PPC3_MOUSE	Q4ppc3 mus musculus

1273	198.5	5.0	830	2	05T145_HUMAN	Q5C145_homo_sapien	1346	195	4.9	262	2	Q720G3_9DIPT	Q720G3_phlebotomus
1274	198.5	5.0	1051	2	05U4U1_XENLA	Q5U4U1_xenopus lae	1347	195	4.9	336	2	Q3V0Q7_MOUSE	Q3V0Q7_mus_musculus
1275	198.5	5.0	1214	2	090YD2_XENLA	Q90YD2_xenopus lae	1348	195	4.9	432	1	UROK_RAT	P29598_rattus norvegicus
1276	198.5	5.0	1289	2	059FL3_HUMAN	Q59FL3_homo_sapien	1349	194.5	4.9	246	1	TRYD_RAT	P00762_rattus norvegicus
1277	198	5.0	235	1	TRYD_HUMAN	Q9BZJ3_homo_sapien	1350	194.5	4.9	246	2	Q9ROT7_MOUSE	Q9ROT7_mus_musculus
1278	198	5.0	235	1	DERF3_DERFA	P49273_dermatophag	1351	194.5	4.9	247	2	Q561Z7_BRAE	Q561Z7_baccharis
1279	198	5.0	261	2	Q6QX60_MAYAXI	Q6QX60_lepeophthei	1352	194.5	4.9	258	2	Q5VAN2_CERO	Q5VAN2_cercocebus
1280	198	5.0	268	2	Q5ISB8_MAYDE	Q5ISB8_mayetiella d	1353	194.5	4.9	261	2	Q725F4_HUMAN	Q725F4_homo_sapien
1281	198	5.0	427	2	Q5DI98_MANSE	Q5DI98_manduca sex	1354	194.5	4.9	278	2	Q4SH19_TETNG	Q4SH19_tetodon n
1282	198	5.0	427	2	Q6Y2X4_MANSE	Q6Y2X4_manduca sex	1355	194.5	4.9	283	2	Q95Y22_GANNE	Q95Y22_lumbricus b
1283	198	5.0	760	1	CO2_MOUSE	P11180_mus_musculus	1356	194.5	4.9	333	1	PLMN_SHEEP	P81286_ovis aries
1284	198	5.0	1024	1	SEZU1_HUMAN	Q3BYH1_homo_sapien	1357	194.5	4.9	339	2	Q28GNI_XENTR	Q28GNI_xenopus tro
1285	198	5.0	1128	2	Q4SG68_TETNG	Q4SG68_tetradodon n	1358	194.5	4.9	339	2	Q4SPG0_TETNG	Q4SPG0_tetradodon n
1286	197.5	5.0	220	2	Q16PJ0_ABDAP	Q16PJ0_aedes aegypt	1359	194.5	4.9	393	2	Q5MPC5_MANSE	Q5MPC5_manduca sex
1287	197.5	5.0	226	1	COGS_UCAPU	P00771_uca_pugilati	1360	194.5	4.9	394	2	Q5TMN0_ANOGA	Q5TMN0_anopheles g
1288	197.5	5.0	242	2	Q6NTB8_HUMAN	Q6NTB8_homo_sapien	1361	194.5	4.9	461	2	Q4VJ74_XENLA	Q4VJ74_xenopus lae
1289	197.5	5.0	246	2	Q6IEB6_RAT	Q6IEB6_rattus norv	1362	194.5	4.9	618	2	Q17317_AEDAE	Q17317_aedes aegypt
1290	197.5	5.0	248	1	KLK12_HUMAN	Q3UK10_homo_sapien	1363	194.5	4.9	1374	2	Q9VSU0_DROME	Q9VSU0_drosophila
1291	197.5	5.0	251	2	Q7Q4H6_ANOGA	Q7Q4H6_anopheles g	1364	194.5	4.9	1449	2	Q9U112_DROME	Q9U112_drosophila
1292	197.5	5.0	255	2	Q96R00_HUMAN	Q96R00_homo_sapien	1365	194.5	4.9	1450	2	Q81Q08_DROME	Q81Q08_drosophila
1293	197.5	5.0	258	2	Q28805_PANTR	Q28805_pan_troglod	1366	194.5	4.9	1458	2	Q1A5L1_BRAE	Q1A5L1_baccharidantio
1294	197.5	5.0	263	2	Q6H319_PIG	Q6H319_sus scrofa	1367	194.5	4.9	1462	2	Q9U113_DROME	Q9U113_drosophila
1295	197.5	5.0	428	2	Q1LV17_BRAE	Q1LV17_brachydantio	1368	194.5	4.9	2382	2	Q9B119_DROME	Q9B119_drosophila
1296	197.5	5.0	752	2	Q3SGZ8_HUMAN	Q3SGZ8_homo_sapien	1369	194.5	4.9	2409	2	Q960G6_DROME	Q960G6_drosophila
1297	197	5.0	222	2	Q91WZ0_RAT	Q91WZ0_rattus norv	1370	194.5	4.9	2428	2	Q816X6_BOOMI	Q816X6_boophilus m
1298	197	5.0	253	2	Q5OBG5_9DIPT	Q5OBG5_culicoides g	1371	194.5	4.9	2549	2	Q2L697_CIOIN	Q2L697_ciona intes
1299	197	5.0	258	2	Q7QKX6_ANOGA	Q7QKX6_anopheles g	1372	194.5	4.9	2786	2	Q9VSU2_DROME	Q9VSU2_drosophila
1300	197	5.0	261	2	Q9VXC7_DROME	Q9VXC7_drosophila	1373	194	4.9	243	2	Q7PF77_ANOGA	Q7PF77_anopheles g
1301	197	5.0	268	2	Q51V42_MAYDE	Q51V42_mayetiella d	1374	194	4.9	245	2	Q42160_PETMA	Q42160_petromyzon
1302	197	5.0	338	1	PLMN_HORSE	P80010_equus caball	1375	194	4.9	247	2	Q70T74_HORSE	Q70T74_equus caball
1303	197	5.0	382	2	Q29KZ8_DROPS	Q29KZ8_drosophila	1376	194	4.9	253	1	Q9VAG3_DROME	Q9VAG3_drosophila
1304	197	5.0	385	2	Q5U365_RAT	Q5U365_rattus norv	1377	194	4.9	259	2	CFAD_PIG	P51779_sus scrofa
1305	197	5.0	421	2	Q9SR86_DROME	Q9SR86_drosophila	1378	194	4.9	276	2	Q16ID2_AEDAE	Q16ID2_aedes aegypt
1306	197	5.0	585	2	Q9U0E2_TRICA	Q9U0E2_trichophila c	1379	194	4.9	301	2	Q16U09_AEDAE	Q16U09_aedes aegypt
1307	197	5.0	745	2	Q91701_XENLA	Q91701_xenopus lae	1380	194	4.9	379	2	Q4SU40_TETNG	Q4SU40_tetradodon n
1308	197	5.0	760	2	Q70J30_MOUSE	Q70J30_mus_musculus	1381	194	4.9	556	2	Q80J35_BRAE	Q80J35_baccharidantio
1309	196.5	5.0	219	2	Q91036_GADMO	Q91036_gadus morhu	1382	194	4.9	578	2	Q3USM6_MOUSE	Q3USM6_mus_musculus
1310	196.5	5.0	223	2	Q297G1_DROPS	Q297G1_drosophila	1383	194	4.9	806	1	PLMN_MACEU	Q18713_macropus eu
1311	196.5	5.0	231	2	Q6GYT5_STRCA	Q6GYT5_struthio ca	1384	193.5	4.9	183	2	Q6PLJ7_9EUC4	Q6PLJ7_fenneopena
1312	196.5	5.0	246	2	Q4SH18_TETNG	Q4SH18_tetradodon n	1385	193.5	4.9	235	2	Q70820_ANOGA	Q70820_anopheles g
1313	196.5	5.0	259	2	Q81RE0_DROME	Q81RE0_drosophila	1386	193.5	4.9	245	2	Q792Y9_MOUSE	Q792Y9_mus_musculus
1314	196.5	5.0	269	1	ELAZB_HUMAN	P88218_homo_sapien	1387	193.5	4.9	246	2	Q9QUR9_MOUSE	Q9QUR9_mus_musculus
1315	196.5	5.0	270	2	Q16JMH_AEDAE	Q16JMH_aedes aegypt	1388	193.5	4.9	247	2	Q6T376_EISFO	Q6T376_eisenla foe
1316	196.5	5.0	298	2	Q8T4N4_RHAP	Q8T4N4_rhipicephal	1389	193.5	4.9	247	2	Q9W705_PAROL	Q9W705_parielichthy
1317	196.5	5.0	362	2	Q566K9_XENTR	Q566K9_xenopus tro	1390	193.5	4.9	256	2	Q27540_CHOPE	Q27540_choristoneu
1318	196.5	5.0	370	2	Q299U3_DROPS	Q299U3_drosophila	1391	193.5	4.9	261	2	Q28Y25_DROPS	Q28Y25_drosophila
1319	196.5	5.0	570	1	BBP3_STRPU	P49013_strongyloce	1392	193.5	4.9	262	2	Q70144_ANOGA	Q70144_anopheles g
1320	196.5	5.0	829	2	Q6NU19_HUMAN	Q6NU19_homo_sapien	1393	193.5	4.9	263	2	Q9V5X7_DROME	Q9V5X7_drosophila
1321	196.5	5.0	2030	2	Q2WBV6_PLADU	Q2WBV6_platyneris	1394	193.5	4.9	269	2	Q5M925_XENTR	Q5M925_xenopus tro
1322	196.5	5.0	2524	1	NOTCH_XENLA	P21783_xenopus lae	1395	193.5	4.9	272	2	Q29Q07_DROME	Q29Q07_drosophila
1323	196	5.0	248	2	Q6GPX7_XENLA	Q6GPX7_xenopus lae	1396	193.5	4.9	317	2	Q9DGR3_XENLA	Q9DGR3_xenopus lae
1324	196	5.0	257	2	Q52KSH_XENLA	Q52KSH_xenopus lae	1397	193.5	4.9	347	2	Q70B73_ANOGA	Q70B73_anopheles g
1325	196	5.0	262	2	Q5XKPS_XENLA	Q5XKPS_xenopus lae	1398	193.5	4.9	375	2	Q28XQ9_DROPS	Q28XQ9_drosophila
1326	196	5.0	270	1	ELAZB_HUMAN	P08861_homo_sapien	1399	193.5	4.9	389	2	Q294U5_DROPS	Q294U5_drosophila
1327	196	5.0	275	2	Q66UC8_9DIPT	Q66UC8_culicoides	1400	193.5	4.9	789	2	Q8N1E9_HUMAN	Q8N1E9_homo_sapien
1328	196	5.0	349	2	Q17N99_AEDAE	Q17N99_aedes aegypt	1401	193.5	4.9	1089	2	Q8T3A0_CIOIN	Q8T3A0_ciona intes
1329	196	5.0	400	2	Q9GRG2_TENMO	Q9GRG2_tenebrio m	1402	193.5	4.9	1235	2	Q6IO50_HUMAN	Q6IO50_homo_sapien
1330	196	5.0	418	2	Q4RJM2_TETNG	Q4RJM2_tetradodon n	1403	193.5	4.9	2471	1	NOTC2_RAT	NOTC2_rattus norv
1331	196	5.0	432	2	Q4XR76_RAT	Q4XR76_rattus norv	1404	193	4.9	239	2	Q30808_EISFO	Q30808_eisenla foe
1332	196	5.0	484	2	Q11V3_9PRIM	Q11V3_gorilla gor	1405	193	4.9	253	1	CAC3_BOVIN	P05805_bos taurus
1333	196	5.0	850	2	Q118Z3_BRAE	Q118Z3_brachydantio	1406	193	4.9	268	1	ELAI_CANFA	Q86780_canis famli
1334	196	5.0	3623	1	CUBN_RAT	Q70244_rattus norv	1407	193	4.9	268	2	Q9XY56_CTEFE	Q9XY56_ctenocephal
1335	195.5	5.0	247	2	Q5H730_MACMU	Q5H730_mecaca mula	1408	193	4.9	269	2	Q95KM7_BOVIN	Q95KM7_bos taurus
1336	195.5	5.0	257	1	GRAM_HUMAN	P51124_homo_sapien	1409	193	4.9	272	2	Q52NWS_9DIPT	Q52NWS_anopheles c
1337	195.5	5.0	267	2	Q9GCP2_DROME	Q9GCP2_drosophila	1410	193	4.9	305	2	Q17106_AEDAE	Q17106_aedes aegypt
1338	195.5	5.0	274	2	Q17086_ANOST	Q17086_anopheles a	1411	193	4.9	315	2	Q5MGE3_LONON	Q5MGE3_iononla obl
1339	195.5	5.0	276	2	Q18443_HELAM	Q18443_hellicoverpa	1412	193	4.9	357	2	Q16L26_AEDAE	Q16L26_aedes aegypt
1340	195.5	5.0	292	2	Q16N48_AEDAE	Q16N48_aedes aegypt	1413	193	4.9	357	2	Q17B40_AEDAE	Q17B40_aedes aegypt
1341	195.5	5.0	752	1	NOT2_PANTR	Q08674_pan_troglod	1414	193	4.9	379	2	Q178V8_AEDAE	Q178V8_aedes aegypt
1342	195.5	5.0	2471	1	NOTC2_HUMAN	Q04721_homo_sapien	1415	193	4.9	392	2	Q1HRE9_AEDAE	Q1HRE9_aedes aegypt
1343	195.5	5.0	2471	2	Q5VTDO_HUMAN	Q5VTDO_homo_sapien	1416	193	4.9	393	2	Q7QAC0_ANOGA	Q7QAC0_anopheles g
1344	195	4.9	242	2	Q4ADVA_SEROU	Q4ADVA_seriola qui	1417	193	4.9	423	2	Q57433_FUGRU	Q57433_fugu rubrip
1345	195	4.9	261	1	KLK1_MOUSE	P15947_mus_musculus	1418	193	4.9	447	2	Q499M3_MOUSE	Q499M3_mus_musculus

1419	193	4.9	481	2	09H284_HUMAN	09h284 homo sapien
1420	193	4.9	543	2	06PHN6_MOUSE	06phn6 mus musculus
1421	193	4.9	601	2	016S05_AEDAE	016s05 aedes aegypti
1422	193	4.9	962	2	08C420_MOUSE	08c420 mus musculus
1423	193	4.9	963	2	06P1D5_MOUSE	06p1d5 mus musculus
1424	193	4.9	1275	2	061PE4_CAEBR	061pe4 caenorhabditis
1425	193	4.9	2030	2	04RHF2_TETNG	04rhf2 tetraodon n
1426	192.5	4.9	178	2	093594_DICLA	093594 dicentrarchus
1427	192.5	4.9	222	2	094508_DERPA	094508 dermatophag
1428	192.5	4.9	243	2	05M976_XENTR	05m976 xenopus tro
1429	192.5	4.9	245	2	05TN68_ANOGA	05tn68 anopheles g
1430	192.5	4.9	246	2	0921R9_MOUSE	0921r9 mus musculus
1431	192.5	4.9	247	2	08NHM4_HUMAN	08nhm4 homo sapien
1432	192.5	4.9	256	1	TRYP_CHOFU	p35042 chorissteneu
1433	192.5	4.9	257	2	04QRH5_BRARE	04qrh5 brachydanio
1434	192.5	4.9	268	2	028276_DROPS	028276 drosophila
1435	192.5	4.9	276	1	KLK11_MOUSE	09qy43 mus musculus
1436	192.5	4.9	381	2	08MOY4_DROME	08my44 drosophila
1437	192.5	4.9	438	2	05RDX7_PONPY	05rdx7 pongo pygma
1438	192.5	4.9	669	2	04SC13_TETNG	04sc13 tetraodon n
1439	192.5	4.9	754	2	P79816_ORYLA	p79816 oryzae lat
1440	192.5	4.9	233	2	07Q344_ANOGA	07q344 anopheles g
1441	192	4.9	244	2	042159_PETWA	042159 petiomysom
1442	192	4.9	246	2	09BL17_LUMBU	09bl17 lumbricus r
1443	192	4.9	254	2	05TWT2_ANOGA	05tw2 anopheles g
1444	192	4.9	254	2	09XY10_RHTDO	09xy10 rhyzopertha
1445	192	4.9	256	2	06MUY6_BDEBA	06my6 bdeliiovibri
1446	192	4.9	265	2	04S848_TETNG	04s848 tetraodon n
1447	192	4.9	304	2	016LRO_AEDAE	016lro aedes aegypti
1448	192	4.9	354	2	07OKL3_ANOGA	07okl3 anopheles g
1449	192	4.9	380	2	09Y1K3_ANOGA	09y1k3 anopheles g
1450	192	4.9	383	2	077102_MANSE	077102 manduca sex
1451	192	4.9	383	2	077102_MANSE	077102 manduca sex
1452	192	4.9	383	2	077102_MANSE	077102 manduca sex
1453	191.5	4.9	235	2	05TXH2_AEDAE	05txh2 aedes aegypti
1454	191.5	4.9	243	2	05M959_XENTR	05m959 xenopus tro
1455	191.5	4.9	247	1	TRYP_HUMAN	p07477 homo sapien
1456	191.5	4.9	247	2	05NV57_HUMAN	05nv57 homo sapien
1457	191.5	4.9	247	2	017039_ANOGA	017039 anopheles g
1458	191.5	4.9	265	2	06QX61_9MAKI	06qx61 lepeophthei
1459	191.5	4.9	270	2	04S520_TETNG	04s520 tetraodon n
1460	191.5	4.9	279	2	0155V8_DERPA	0155v8 dermatophag
1461	191.5	4.9	281	2	076898_DROME	076898 drosophila
1462	191.5	4.9	284	2	081RX5_DROME	081rx5 drosophila
1463	191.5	4.9	285	2	07Q298_ANOGA	07q298 anopheles g
1464	191.5	4.9	316	2	08SX48_DROPS	08sx48 drosophila
1465	191.5	4.9	360	2	08SX54_DROME	08sx54 drosophila
1466	191.5	4.9	385	2	08SX51_DROME	08sx51 drosophila
1467	191.5	4.9	480	2	06G1T1_KENLA	06g1t1 xenopus lae
1468	191.5	4.9	733	2	080TP0_MOUSE	080tp0 mus musculus
1469	191.5	4.9	830	1	LYAM3_HUMAN	lyam3 homo sapien
1470	191.5	4.9	897	1	Q3V6S1_MOUSE	q3v6s1 mus musculus
1471	191.5	4.9	2468	2	0800B4_BRARE	0800b4 brachydanio
1472	191.5	4.9	3396	2	09VM55_DROME	09vm55 drosophila
1473	191	4.8	228	2	06PEJ8_HUMAN	06pej8 homo sapien
1474	191	4.8	230	2	04RQD7_TETNG	04rqd7 tetraodon n
1475	191	4.8	248	2	05H732_MACMU	05h732 macaca mula
1476	191	4.8	254	1	KLK4_HUMAN	09y5k2 homo sapien
1477	191	4.8	255	1	Q25227_LUCCU	025227 lucilia cup
1478	191	4.8	256	2	081B85_9DIPT	081b85 ochlerotatu
1479	191	4.8	270	2	017B83_AEDAE	017b83 aedes aegypti
1480	191	4.8	273	2	051Y40_MAYBE	051y40 mayetioida
1481	191	4.8	277	2	081Q10_DROME	081q10 drosophila
1482	191	4.8	282	2	04VB11_BRARE	04vb11 brachydanio
1483	191	4.8	317	2	08K4D1_MOUSE	08k4d1 mus musculus
1484	191	4.8	317	2	08K4I7_MOUSE	08k4i7 mus musculus
1485	191	4.8	415	2	09GRM0_HOUDI	09grm0 holocorichia
1486	191	4.8	646	2	Q29097_2IG	Q29097 sus scrofa
1487	191	4.8	758	2	Q6MG73_RAT	Q6mg73 rattus norv
1488	191	4.8	1006	2	Q29D77_DROPS	Q29d77 drosophila
1489	190.5	4.8	245	2	Q4G0C2_MOUSE	Q4g0c2 mus musculus
1490	190.5	4.8	246	2	Q3V2G3_MOUSE	Q3v2g3 mus musculus
1491	190.5	4.8	246	2	Q792Z0_MOUSE	Q792z0 mus musculus

1492	190.5	4.8	257	2	081BE3_9DIPT	081be3 aedes polyn
1493	190.5	4.8	314	2	Q28EV7_XENTR	Q28ev7 xenopus tro
1494	190.5	4.8	317	2	Q5PEM3_XENTR	Q5pem3 xenopus tro
1495	190.5	4.8	360	2	Q17HM7_AEDAE	Q17hm7 aedes aegypti
1496	190.5	4.8	579	1	MFRP_HUMAN	Q9by79 homo sapien
1497	190.5	4.8	762	2	Q9YIC6_CYPCA	Q9yic6 cyprinus ca
1498	190.5	4.8	768	1	LYAM3_MOUSE	Q01102 mus musculus
1499	190.5	4.8	768	2	Q32MFI_MOUSE	Q32mfi mus musculus
1500	190.5	4.8	1064	1	FBP1_STRPU	P10079 stiongyloce

ALIGNMENTS

RESULT 1

Q6UXH9_HUMAN PRELIMINARY; PRT; 720 AA.

Q6UXH9; ID

AC Q6UXH9; AC

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 02-MAY-2006, entry version 14.

DE ELGCE699.

GN ORFNames=UNC699;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhina;

OC Catarrhini; Hominoidea; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22867296; PubMed=1295309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gunney A.L., Abaya E., Baker K., Baldwin D.T., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Dewell P., Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Helens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schonfeld J., Sesbagli S., Simmons L., Singh J., Smith V., Stinson J., Vagstad A., Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H., Yandura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D., Wood W.I., Godowski P.J., Gray A.M.;

RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."

RL Genome Res. 13:2265-2270(2003).

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CC EMBL: AY358346; AAC08712.1; -; mRNA.

DR UniGene: Hs.55044; -.

DR HSSP: P00734; IBB0.

DR Ensembl: ENSG00000149090; Homo sapiens.

DR GO: GO:0004252; F:serine-type endopeptidase activity; IEA.

DR GO: GO:0006508; P:proteolysis; IEA.

DR InterPro: IPR000859; CUB.

DR InterPro: IPR006210; EGF.

DR InterPro: IPR000742; EGF_3.

DR InterPro: IPR006209; EGF-like.

DR InterPro: IPR013032; EGF-like reg.

DR InterPro: IPR009003; Pept_Ser_Cys.

DR InterPro: IPR001254; Peptidase_S1_56.

DR InterPro: IPR001314; Peptidase_S1A.

DR Pfam: PF00431; CUB; 1.

DR Pfam: PF00008; EGF; 1.

DR Pfam: PF00084; Sushi; 1.

DR Pfam: PF00089; Trypsin; 1.

DR PRINTS: PR00722; CHYMOTRYPSIN.

DR SMART: SM00032; CCP; 2.

DR SMART: SM00042; CUB; 1.

DR SMART: SM00181; EGF; 2.

DR SMART: SM00020; Tryp_SPC; 1.

DR PROSITE: PS01180; CUB; 1.

DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50923; SUSH1; 2.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
SQ SEQUENCE 720 AA; 80199 MW; DC898BC241289D3 CRC64;

Query Match 100.0%; Score 3945; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 3, 8e-288;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 VVGTTIPCCNNEECSCLIHPGCTIFENCKSCRNSWGTLDDFVYKGFYCAECRAGW 120
DB 61 VVGTTIPCCNNEECSCLIHPGCTIFENCKSCRNSWGTLDDFVYKGFYCAECRAGW 120
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DB 121 YGDCMRCGCVLRAPKQIILLESYPLNAHCWMTTHAKPGFVIQLRFVMLSLEFDYMCQYD 180
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DB 121 YGDCMRCGCVLRAPKQIILLESYPLNAHCWMTTHAKPGFVIQLRFVMLSLEFDYMCQYD 180
QY 181 YVEVRDGNDRDQIIRKVCNERNPAPIQSIGSSLHVLPHSDGSKNPDGFHAYIEBITACS 240
DB 181 YVEVRDGNDRDQIIRKVCNERNPAPIQSIGSSLHVLPHSDGSKNPDGFHAYIEBITACS 240
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DB 241 SSPCFHGTGCVLDKAGSYKACLAGYTGRCENILLEERNCSDPGPNVGYOKITGGGGLI 300
QY 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIAKCEPKISDLVRRVYL 360
DB 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIAKCEPKISDLVRRVYL 360
QY 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIAKCEPKISDLVRRVYL 360
DB 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIAKCEPKISDLVRRVYL 360
QY 361 PMQVOSRETPHLQLYSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAF 420
DB 361 PMQVOSRETPHLQLYSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAF 420
QY 421 RLSSRRCTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLKMPQAAIYRRTSGVHDSGL 480
DB 421 RLSSRRCTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLKMPQAAIYRRTSGVHDSGL 480
QY 481 HKGMFLVCSGALVNERTVVAHCVTDLGKVTMIKTADLKVVLGKFFRDDDRDEKTIQS 540
DB 481 HKGMFLVCSGALVNERTVVAHCVTDLGKVTMIKTADLKVVLGKFFRDDDRDEKTIQS 540
QY 541 LQISAIIILHPYDPIILLDADIAIILKLDKARISTRVOPICLAASRDISTSFQESHITVAG 600
DB 541 LQISAIIILHPYDPIILLDADIAIILKLDKARISTRVOPICLAASRDISTSFQESHITVAG 600
QY 601 MNVLADVRSPGKNDTLRSVSVVDSILCEQHEDHGIPIVSYVDNMFCAWETPA9SDI 660
DB 601 MNVLADVRSPGKNDTLRSVSVVDSILCEQHEDHGIPIVSYVDNMFCAWETPA9SDI 660
QY 661 CTAETGGIAAASPGRASPBPBMHLMGLVSNKYDCTCSHSLSTAFYTKVLPRKDIERNMK 720
DB 661 CTAETGGIAAASPGRASPBPBMHLMGLVSNKYDCTCSHSLSTAFYTKVLPRKDIERNMK 720

RESULT 2
OSUPI4 HUMAN PRELIMINARY; PRT; 720 AA.
AC OSUPI4,
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DE 02-MAY-2006, entry version 7.
DE Hypothetical protein DKFP667H2312.
OS Name=DKFP667H2312;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph node;
RA The German cDNA Consortium;
RA Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Pobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.

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CC EMBL; AL632391; CA146203.1; -; mRNA.
CC Ensemble; ENSG00000149090; Homo sapiens.

DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.

DR InterPro; IPR000859; CUB.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR009003; pepf_ser_Cys.
DR InterPro; IPR01254; peptidase_S1_96.
DR InterPro; IPR001314; peptidase_S1A.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sush1; 2.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.

DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00020; TYP_SPC; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50923; SUSH1; 2.
DR PROSITE; PS50240; TRYPsin_DOM; 1.

KW Hypothetical protein.
SQ SEQUENCE 720 AA; 80227 MW; 1C8A8A8C4BEE7767 CRC64;

Query Match 99.9%; Score 3941; DB 2; Length 720;
Best Local Similarity 99.9%; Pred. No. 7, 7e-288;
Matches 719; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MELGCMWQLGTLFTQLLLISLPREYTVINEACPGAEWNIWCRECEYDQIECVCPGKRE 60
QY 61 VVGTTIPCCNNEECSCLIHPGCTIFENCKSCRNSWGTLDDFVYKGFYCAECRAGW 120
DB 61 VVGTTIPCCNNEECSCLIHPGCTIFENCKSCRNSWGTLDDFVYKGFYCAECRAGW 120
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DB 121 YGDCMRCGCVLRAPKQIILLESYPLNAHCWMTTHAKPGFVIQLRFVMLSLEFDYMCQYD 180
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DB 121 YGDCMRCGCVLRAPKQIILLESYPLNAHCWMTTHAKPGFVIQLRFVMLSLEFDYMCQYD 180
QY 181 YVEVRDGNDRDQIIRKVCNERNPAPIQSIGSSLHVLPHSDGSKNPDGFHAYIEBITACS 240
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QY 361 PMQVOSRETPHLQLYSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAF 420
DB 361 PMQVOSRETPHLQLYSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAF 420

OX NCBI_TaxId=9606;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RX TISSUE=Chondrosarcoma Lung Metastasis;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Piarne C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Mowley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehey J., Hulton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Wyere R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalek U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.U.M., Matra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RC NUCLEOTIDE SEQUENCE.
 RX TISSUE=Chondrosarcoma Lung Metastasis;
 RA Director MGC Project;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: BC089434; AAH89434.1; -; mRNA.
 DR UniGene; Hs.55044; -.
 DR MEROPS; S01.998; -.
 DR Ensembl; ENSG00000149090; Homo sapiens.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
 DR GO; GO:0006508; F:proteolysis; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR013032; EGF_like_reg.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00084; Sushi; 2.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PSS0923; SUS_H; 2.
 DR PROSITE; PSS0240; TRYP_SIN_DOM; 1.
 DR PROSITE; PSS0240; TRYP_SIN_DOM; 1.
 KW Protease.
 SQ SEQUENCE 737 AA; 81943 MW; PD3BACCFE47778FE CRC64;

Query March 99.5%; Score 3926.5; DB 2; Length 737;
 Best Local Similarity 97.7%; Pred. No. 9.8e-287;
 Matches 720; Conservative 0; Mismatches 0; Indels 17; Gaps 1;
 1 MELGCWTQGLTFLQLLTSLPREYTVINACPGAEWNIMGCECEYDQIEVCVCKR 60

Db 1 MELGCWTQGLTFLQLLTSLPREYTVINACPGAEWNIMGCECEYDQIEVCVCKR 60
 QY 61 VVGYYTTPCCRNENEDSCLIHPGCTIFENCKSCRGSGGTTDDPYVKGFTYACBRAG 120
 Db 61 VVGYYTTPCCRNENEDSCLIHPGCTIFENCKSCRGSGGTTDDPYVKGFTYACBRAG 120
 QY 121 YGGDCRCGCVLAAPKQGLILLESYPINACEWTHAKPGVQLRFVMLSLBEDYMCQYD 180
 Db 121 YGGDCRCGCVLAAPKQGLILLESYPINACEWTHAKPGVQLRFVMLSLBEDYMCQYD 180
 QY 181 YVEVRDGNRNDGQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNDFGFAIYEETTACS 240
 Db 181 YVEVRDGNRNDGQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNDFGFAIYEETTACS 240
 QY 241 SSPCFHDTGTCVLDKAGSYKACLAGYTGQRCENL-----LEERNCSDP 283
 Db 241 SSPCFHDTGTCVLDKAGSYKACLAGYTGQRCENL-----LEERNCSDP 283
 QY 284 GGPVNGYOKITGGPGLINGRHAIGTVSPFCNNSYVLSGNEKRTCOQNGEMSGKQPICT 343
 Db 301 GGPVNGYOKITGGPGLINGRHAIGTVSPFCNNSYVLSGNEKRTCOQNGEMSGKQPICT 360
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 QY 404 QHHTLOQYECISPFYRRLGLSSRRCTCLRTCKMGRAPSCPTIGKTIENITAPTKQIRMP 463
 Db 421 QHHTLOQYECISPFYRRLGLSSRRCTCLRTCKMGRAPSCPTIGKTIENITAPTKQIRMP 480
 QY 464 WQAIYRRTSGVNDGSLHKAMFLVCSGALVNRVTVAACHCTDGLKVTMTADLKV 523
 Db 481 WQAIYRRTSGVNDGSLHKAMFLVCSGALVNRVTVAACHCTDGLKVTMTADLKV 540
 QY 524 LGRFYRDDDEKTIQSLQISAIILHPNYDPIILDDIALIKLIDKARISTRVQPICLAA 583
 Db 541 LGRFYRDDDEKTIQSLQISAIILHPNYDPIILDDIALIKLIDKARISTRVQPICLAA 600
 QY 584 SRDLSTFSQSHITTVAGMNVLAIVRSFGFNQDLIRSGVSVVDSLCEEBHEHGHIPVS 643
 Db 601 SRDLSTFSQSHITTVAGMNVLAIVRSFGFNQDLIRSGVSVVDSLCEEBHEHGHIPVS 660
 QY 644 TDNMFCAWERTAPSDICTAETGIAVSPGRASPEPRHMLGLVMSYDXTCSHRLST 703
 Db 661 TDNMFCAWERTAPSDICTAETGIAVSPGRASPEPRHMLGLVMSYDXTCSHRLST 720
 QY 704 AFTKVLPEFKDMIRNMK 720
 Db 721 AFTKVLPEFKDMIRNMK 737
 RESULT 5
 Q96JW2 HUMAN PRELIMINARY; PRT; 737 AA.
 ID Q96JW2 HUMAN PRELIMINARY; PRT; 737 AA.
 AC Q96JW2;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 02-MAY-2006, entry version 1.
 DE CDNA FLJ14935 f1s, clone PLACE1009992, weakly similar to LIMULUS
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhina;
 CC Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RX TISSUE=Placenta;
 PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Ohtsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohayashi M., Nishitani T., Shibahata T., Tanaka T., Itoh S.,

RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwanaga T., Magatsuna M., Shiratori A.,
RA Sudo H., Hasegiri T., Kaku Y., Kodaïra H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Niinomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimura M., Watanabe M., Hirao K., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Horita T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Masehino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Oho T., Yamada K., Fujii K., Ozaki K., Hiroo M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senda T.,
RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Muzushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
CNAs.";
RL Nat. Genet. 36:40-45(2004).
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CC
CC EMBL, AK027811, BAB5540.1; -, mRNA.
DR HSP, P00736; IGP2.
DR MEROP, S01.998; -.
DR Ensemble1, ENSG00000149090; Homo sapiens.
DR GO, GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO, GO:0006508; P:proteolysis; IEA.
DR InterPro, IPR000859; CUB.
DR InterPro, IPR006210; EGF.
DR InterPro, IPR000742; EGF_3.
DR InterPro, IPR006209; EGF_like.
DR InterPro, IPR013033; EGF_like_reg.
DR InterPro, IPR009003; Pept_Ser_Cys.
DR InterPro, IPR001254; Peptidase_S1_S6.
DR InterPro, IPR001314; Peptidase_S1A.
DR InterPro, IPR000436; Sushi_SCR_CCP.
DR Pfam, PF00431; CUB; 1.
DR Pfam, PF00008; EGF; 1.
DR Pfam, PF00008; Sushi; 2.
DR Pfam, PF00084; Trypsin; 1.
DR PRINTS, PR00722; CHYMOTRYPSIN.
DR SMART, SM00032; CCP; 2.
DR SMART, SM00042; CUB; 1.
DR SMART, SM00181; EGF; 2.
DR SMART, SM00020; TYP_Spc; 1.
DR PROSITE, PS01180; CUB; 1.
DR PROSITE, PS00022; EGF_1; 1.
DR PROSITE, PS01186; EGF_2; 1.
DR PROSITE, PS00026; EGF_3; 1.
DR PROSITE, PS00923; SUSI; 2.
DR PROSITE, PS0240; TRYPSIN_DOM; 1.
DR PROSITE, PS0240; TRYPSIN_DOM; 1.
SQ SEQUENCE 737 AA; 81953 MW; 4F51689CEB32B44 CRC64;

Query Match 99.4%; Score 3921.5; DB 2; Length 737;
Best Local Similarity 97.6%; Pred. No. 2,3e-286;
Matches 719; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

QY 1 MELCWTQGLTFLQILLISLPREYVYNACGAEWNIWCRCECEJDEJECVCPKRE 60
DB 1 MELCWTQGLTFLQILLISLPREYVYNACGAEWNIWCRCECEJDEJECVCPKRE 60
QY 61 VVGTTICCRNEBNECDSCLIHPGCTIFENCKSCRNWSGGLTDDFYVKGTYCAECRA 120

DB 61 VVGTTICCRNEBNECDSCLIHPGCTIFENCKSCRNWSGGLTDDFYVKGTYCAECRA 120
QY 121 YGGDCNRCQGVLPAPKQGLILLESYPINACEWTHAKPGVQLRFVWLSEFDYMCQYD 180
DB 121 YGGDCNRCQGVLPAPKQGLILLESYPINACEWTHAKPGVQLRFVWLSEFDYMCQYD 180
QY 181 YVEVRGDNRRDQGIIRVCGNERPAPIQSIGSSLHLVPHSDGSKNDFGHAITYEETACS 240
DB 181 YVEVRGDNRRDQGIIRVCGNERPAPIQSIGSSLHLVPHSDGSKNDFGHAITYEETACS 240
QY 241 SSPCFHDGTCVLDKAGSYCACIAGTGORCEUL-----LEERNCSDP 283
DB 241 SSPCFHDGTCVLDKAGSYCACIAGTGORCEUL-----LEERNCSDP 300
QY 284 GGPVNGYOKITGPGGLINGHAKITGVVSFFCNNSVYLSGNEKRTCOQNGWSKOPICI 343
DB 301 GGPVNGYOKITGPGGLINGHAKITGVVSFFCNNSVYLSGNEKRTCOQNGWSKOPICI 360
QY 344 KACREPKISDLYRRVLPVQVQSERETPLHQLYSAAFSKQLOAPTKCPALPGDLPNGY 403
DB 361 KACREPKISDLYRRVLPVQVQSERETPLHQLYSAAFSKQLOAPTKCPALPGDLPNGY 420
QY 404 QHLHTLOVECTSPFRRIGSSRRCTLRGKXSGRAPSCIPICGKIENTITAPKTOGLRWP 463
DB 421 QHLHTLOVECTSPFRRIGSSRRCTLRGKXSGRAPSCIPICGKIENTITAPKTOGLRWP 480
QY 464 WQAAIYRRTSGVHDSGLHKAMFLVCSGALVNERTVVAACVTDGKVTMKTADLVK 523
DB 481 WQAAIYRRTSGVHDSGLHKAMFLVCSGALVNERTVVAACVTDGKVTMKTADLVK 540
QY 524 LGRFYRDDDRDEKTIQSLQISAILHPNDPILLDADIALKLDYARISTRVQPICLA 583
DB 541 LGRFYRDDDRDEKTIQSLQISAILHPNDPILLDADIALKLDYARISTRVQPICLA 600
QY 584 SRLSTSPFQESHITVAGMNVADVRSRPGFNDTLRGVSVVNDLSICEQHEHGI PVSV 643
DB 601 SRLSTSPFQESHITVAGMNVADVRSRPGFNDTLRGVSVVNDLSICEQHEHGI PVSV 660
QY 644 TDNNFCAWEPAPSDICTAETGCIAAVSPFGASRDEPRHMLGLVSWSYDKTCSRRLST 703
DB 661 TDNNFCAWEPAPSDICTAETGCIAAVSPFGASRDEPRHMLGLVSWSYDKTCSRRLST 720
QY 704 APTKVLPEKDWIERNNK 720
DB 721 APTKVLPEKDWIERNNK 737
RESULT 6
Q5RD11_PONPY PRELIMINARY; PRT; 720 AA.
ID Q5RD11_PONPY PRELIMINARY; PRT; 720 AA.
AC Q5RD11_PONPY PRELIMINARY; PRT; 720 AA.
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DT 02-MAY-2006, entry version 8.
DE Hypothetical protein DKFZP468N1810.
GN Name=DKFZP468N1810;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhina;
OC Catarrhini; Hominoidea; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Heart;
RG The German CDNA Consortium;
RA Oetemaelder B., Obermaier B., Deutschenbauer S., Schaipp A.,
RA Mewes H.W., Weill B., Amlid C., Oanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBS databases.
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DR EMBL; CR857928; CAH90176.1; -, mRNA.
 DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis; IEA.
 DR InterPro; IPR000858; CUB.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR007442; EGF_3.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR013032; EGF_like_reg.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000436; Sush1_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00004; Sush1; 2.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS00923; SUSH1; 2.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 720 AA; 80041 MW; 3F83E2DAD41F4117 CRC64;
 Query March 98.8%; Score 3898; DB 2; Length 720;
 Best Local Similarity 98.8%; Pred. No. 1.3e-264;
 Matches 709; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 MELGCMWQLGTLFQLLLISLPREYVINEACFGAEWNINCRECEYDQIECVCPGKRE 60
 DB 1 MELGCMWQLGTLFQLLLISLPREYVINEACFGAEWNINCRECEYDQIECVCPGKRE 60
 QY 61 VVGITTCRCRNEECSCLIHPGCTTFENCKSRNGSGTLDFFVYKGFYCAECRAGW 120
 DB 61 VVGITTCRCRNEECSCLIHPGCTTFENCKSRNGSGTLDFFVYKGFYCAECRAGW 120
 QY 121 YGDCMRCGQYLRAPKQIILLESYPLNAHCMTIHAKEGFIQLRFVWLSLEPYMCQYD 180
 DB 121 YGDCMRCGQYLRAPKQIILLESYPLNAHCMTIHAKEGFIQLRFVWLSLEPYMCQYD 180
 QY 181 YVEVRDGDNRDQIIRKVCNRPAPIQSGSSLHVLPHSDGSKNPDGFHA1YEETACS 240
 DB 181 YVEVRDGDNRDQIIRKVCNRPAPIQSGSSLHVLPHSDGSKNPDGFHA1YEETACS 240
 QY 241 YVEVRDGDNRDQIIRKVCNRPAPIQSGSSLHVLPHSDGSKNPDGFHA1YEETACS 240
 DB 241 YVEVRDGDNRDQIIRKVCNRPAPIQSGSSLHVLPHSDGSKNPDGFHA1YEETACS 240
 QY 241 SSPCFHGTGVLDRAGSYKCACLAGYQRCENLLEENCGSDPGGPVNGYQKITGPGELI 300
 DB 241 SSPCFHGTGVLDRAGSYKCACLAGYQRCENLLEENCGSDPGGPVNGYQKITGPGELI 300
 QY 301 NGRRAKIGTVVSPFCNNSYVLSENGEKRTCOQNGEMSGKOPICIRACREPKISDLVRRVYL 360
 DB 301 NGRRAKIGTVVSPFCNNSYVLSENGEKRTCOQNGEMSGKOPICIRACREPKISDLVRRVYL 360
 QY 361 PMQVQSRPTLHQLYSAAFSKQKLQSAFTKKPALPFGDLPMGYQLHTQLQYECISPFYR 420
 DB 361 PMQVQSRPTLHQLYSAAFSKQKLQSAFTKKPALPFGDLPMGYQLHTQLQYECISPFYR 420
 QY 421 RLGSRRRTCLRTGKMSGAPSCIPICGKIENITAPKTGGLWPMQALYRRTSGVHDSL 480
 DB 421 RLGSRRRTCLRTGKMSGAPSCIPICGKIENITAPKTGGLWPMQALYRRTSGVHDSL 480
 QY 481 HKGAMFLVCSGALVNERTVVAACVTDLGKVTMTKTADLKVVYKGFRRDDRDDEKTQS 540
 DB 481 HKGAMFLVCSGALVNERTVVAACVTDLGKVTMTKTADLKVVYKGFRRDDRDDEKTQS 540
 QY 541 LQISAIIHPNVDPILLDADIAIILKLDKARISTRVQPICLAASRLSTSFQESHITVAG 600
 DB 541 LQISAIIHPNVDPILLDADIAIILKLDKARISTRVQPICLAASRLSTSFQESHITVAG 600

QY 601 MNVLADVRSPGPNKDLRSVSVSDSLCEQHEHGI PVSYTDNMFCASWEPTAPSDI 660
 DB 601 MNVLADVRSPGPNKDLRSVSVSDSLCEQHEHGI PVSYTDNMFCASWEPTAPSDI 660
 QY 661 CTAEATGIAVSPFGASPEPRMHLGLVSWSDKTCSHSLSTAFTKVLFPKMIERNMK 720
 DB 661 CTAEATGIAVSPFGASPEPRMHLGLVSWSDKTCSHSLSTAFTKVLFPKMIERNMK 720

RESULT 7
 Q5E9P5 BOVIN PRELIMINARY; PRT; 720 AA.
 AC Q5E9P5;
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 DT 18-APR-2006, entry version 8.
 DE Regeneration associated muscle protease isoform b.
 GN Name=DKFZP586H2123;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Poolled.
 RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
 RA Smith T.P.L., Grose W.M., Freking B.A., Roberts A.J., Stone R.T.,
 Raas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
 Heaton M.P., Laegreid W.M., Rohrer G.A., Chikow-Mckown C.G.,
 Porter G., Holt I., Karaymcheva S., Liang F., Quackenbush J.,
 Keefe J.W.;
 RA "Sequence evaluation of four pooled-tissue normalized bovine CDNA
 RT libraries and construction of a gene index for cattle.";
 RL Genome Res. 11:626-630(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Poolled.
 RA Harnay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keefe J.W.,
 RA Snelling W.M., Weidmann R.T., Smith T.P.L.;
 RT "Sequencing and analysis of Bos taurus full-length insert cDNA
 RT clones.";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

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 CC -----
 CC EMBL; BT020875; AAX08892.1; -, mRNA.
 DR UniGene; Bt.6021; -.
 DR MEROPS; S01.998; -.
 DR GO; GO:0008233; P:peptidase activity; IEA.
 DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR013032; EGF_like_reg.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000436; Sush1_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00004; Sush1; 2.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS01180; CUB; 1.

DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS00923; SUSH1; 2.
 DR PROSITE; PS00240; TRYPsin_DOM; 1.
 KM PROTEASE.
 SQ SEQUENCE 720 AA; 80057 MW; 69DA098FF95037E1 CRC64;
 Query Match 91.7%; Score 3616; DB 2; Length 720;
 Best Local Similarity 90.6%; Pred. No 2.4e-263;
 Matches 652; Conservative 30; Mismatches 38; Indels 0; Gaps 0;
 QY 1 MELGCTQTGLTLPQLLLISSLPREYTVINACGAGMNMCECCEDYDIECVGPKRE 60
 1 MELGMPQLGLAFQLLLISSLPREYTVINACGAGMNMCECCEDYDIECVGPKRE 60
 DB 1 MELGMPQLGLAFQLLLISSLPREYTVINACGAGMNMCECCEDYDIECVGPKRE 60
 QY 61 VNGYTTIPCCNNEECSCLIHQCTTFENCKSRNGSGGTLDDFYVKGPCYCAECRAG 120
 61 VNGYTTIPCCNNEECSCLIHQCTTFENCKSRNGSGGTLDDFYVKGPCYCAECRAG 120
 DB 61 VNGYTTIPCCNNEECSCLIHQCTTFENCKSRNGSGGTLDDFYVKGPCYCAECRAG 120
 QY 121 YGSDCMRCGQVLRAPKQIILLESYPLNACGEMTHAKPGFVIOIRFVMSLEFDYMGQYD 180
 121 YGSDCMRCGQVLRAPKQIILLESYPLNACGEMTHAKPGFVIOIRFVMSLEFDYMGQYD 180
 DB 121 YGSDCMRCGQVLRAPKQIILLESYPLNACGEMTHAKPGFVIOIRFVMSLEFDYMGQYD 180
 QY 181 YVEVRDGDNRDQIIRKVCNENRPAPIQSISSILHVLHSDGSKNDFGFAIYEETAC 240
 181 YVEVRDGDNRDQIIRKVCNENRPAPIQSISSILHVLHSDGSKNDFGFAIYEETAC 240
 DB 181 YVEVRDGDNRDQIIRKVCNENRPAPIQSISSILHVLHSDGSKNDFGFAIYEETAC 240
 QY 241 SSGCFHDGTCVLDKASGYKACLAGYTGRCENILLEERNCSDPGPNVGYOKITGGPGLI 300
 241 SSGCFHDGTCVLDKASGYKACLAGYTGRCENILLEERNCSDPGPNVGYOKITGGPGLI 300
 DB 241 SSGCFHDGTCVLDKASGYKACLAGYTGRCENILLEERNCSDPGPNVGYOKITGGPGLI 300
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 301 NGHAKIGTVSPFCNNSVYLSGNEKRTCOONGHWSKQICICAKCEPKISDLVRRRL 360
 DB 301 NGHAKIGTVSPFCNNSVYLSGNEKRTCOONGHWSKQICICAKCEPKISDLVRRRL 360
 QY 361 PMQVQSERETPLHLYSAFQKQIDAPTKKPVLPFDLPGYOHHTQYECISPFYR 420
 361 PMQVQSERETPLHLYSAFQKQIDAPTKKPVLPFDLPGYOHHTQYECISPFYR 420
 DB 361 PMQVQSERETPLHLYSAFQKQIDAPTKKPVLPFDLPGYOHHTQYECISPFYR 420
 QY 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENTAPKTOGLRMPQAAIYRTSGVHDSL 480
 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENTAPKTOGLRMPQAAIYRTSGVHDSL 480
 DB 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENTAPKTOGLRMPQAAIYRTSGVHDSL 480
 QY 481 HKGAWFLVSGALVNESTVVAACHCTDIAKTMITKADIAKVLGKRYRDDDEKTIQS 540
 481 HKGAWFLVSGALVNESTVVAACHCTDIAKTMITKADIAKVLGKRYRDDDEKTIQS 540
 DB 481 HKGAWFLVSGALVNESTVVAACHCTDIAKTMITKADIAKVLGKRYRDDDEKTIQS 540
 QY 541 LQISATILHNPYDILDLADIAIKLIDKARISTRVOPICLAASRLDSTFSQESHITVAG 600
 541 LQISATILHNPYDILDLADIAIKLIDKARISTRVOPICLAASRLDSTFSQESHITVAG 600
 DB 541 LQISATILHNPYDILDLADIAIKLIDKARISTRVOPICLAASRLDSTFSQESHITVAG 600
 QY 541 LRISATILHNPYDILDLADIAIKLIDKARISTRVOPICLAASRLDSTFSQESHITVAG 600
 541 LRISATILHNPYDILDLADIAIKLIDKARISTRVOPICLAASRLDSTFSQESHITVAG 600
 DB 541 LRISATILHNPYDILDLADIAIKLIDKARISTRVOPICLAASRLDSTFSQESHITVAG 600
 QY 601 MNVLADVRSPGFNDTLRSQVSVVDSLCEQHEHGHIPVSYTDNMFCAWEPAPSDI 660
 601 MNVLADVRSPGFNDTLRSQVSVVDSLCEQHEHGHIPVSYTDNMFCAWEPAPSDI 660
 DB 601 MNVLADVRSPGFNDTLRSQVSVVDSLCEQHEHGHIPVSYTDNMFCAWEPAPSDI 660
 QY 661 CTAFETGGIAVSPGRASPEPRMHLGLVWSYDITKTSRHLSTAFKVLFPKMIERNMK 720
 661 CTAFETGGIAVSPGRASPEPRMHLGLVWSYDITKTSRHLSTAFKVLFPKMIERNMK 720
 DB 661 CTAFETGGIAVSPGRASPEPRMHLGLVWSYDITKTSRHLSTAFKVLFPKMIERNMK 720
 RESULT 8
 OBBU25_MOUSE PRELIMINARY; PRT; 720 AA.
 AC OBBU25;
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 18-APR-2006, entry version 27.
 DE 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched
 DE library, clone:843002G05 product:hypothetical EGF-like domain, CUB
 DE domain, Sushi domain / SCF repeat / CCP module and Serine proteases,
 DE tryptin family domain containing protein, full insert sequence.
 GN Name=E430002G05Rik;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ND; TISSUE=Thymus;
 RX MEDLINE=99219253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RT "High-efficiency full-length cDNA cloning."
 RL Methods Enzymol. 303:19-44(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ND; TISSUE=Thymus;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
 Davis M.J., Wilmom L.G., Aidinis V., Allen J.E.,
 Ambesi-Impombato A., Apweiler R., Attalaya R.N., Bailey T.L.,
 Banasi M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 Chiu K.P., Choudhary V., Christofels A., Clutierbeck D.R.,
 Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 di Bernardo D., Down T., Engstrom P., Faggiolini M., Faulkner G.,
 Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 Hill D., Hummelbeck L., Iacono M., Ieko K., Iwama A., Ishikawa T.,
 Jaki M., Kanapin A., Katoh M., Kawasawa Y., Kello J., Kitamura H.,
 Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 Liun S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 Mouteregi-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
 Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 Okazaki Y., Orlando V., Pang K.C., Pavan M.J., Pavoni G., Pesole G.,
 Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 Rost B., Ruan Y., Salzberg S.L., Sanderlin A., Schneider C.,
 Schonbach C., Sekiguchi K., Sempke C.A., Sene S., Sessa L., Sheng Y.,
 Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 Tamaoka K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 Yamashita H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 Gilmord S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 Wahlestedt C., Maticic J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arai K.,
 Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Niimura N.,
 Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome."
 RL Science 309:1159-1563(2005).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ND; TISSUE=Thymus;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RA RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome."
 RL Science 309:1564-1566(2005).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ND; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Nakada I., Osato N., Saito R., Suzuki H., Yamashita I., Kiyosawa H.,
 Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 Baldarelli R., Hill D.P., Bult C., Hume D.A., Schenckhush J.,
 Schirmel L.M., Kanpin A., Matsuda H., Batalov S., Beisel K.W.,
 Blake J.A., Brad D., Brusio V., Ciothia C., Cordani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaesslerland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Gimond S., Guetlich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A.,
 RA Maglot D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravaei T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Varotto R., Wagner L., Wanstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Yasunishi Y., Konno H., Adachi U., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaesslerland T., Gissi C., King B., Kochava H.,
 RA Kuehl P., Lewis S., Matsuo Y., Mikalido I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Baren G.,
 RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kanliya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hironaka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Konda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akiba S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
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 CC
 DR EMBL, AK088017, BAC40098.1; -; mRNA.
 DR HSSP, P00736, 1GPZ.
 DR MEROPS, S01.998; -.
 DR Ensembl, ENSMUSG00000027188; Mus musculus.
 DR MGI, MGI:2445082; E430002G05Rik.
 DR GO, GO:0005615; C:extracellular space; RCA.
 DR GO, GO:0004263; F:chymotrypsin activity; RCA.
 DR GO, GO:0004295; F:trypsin activity; RCA.
 DR GO, GO:0006508; P:proteolysis; RCA.
 DR InterPro, IPR000859; CUB.
 DR InterPro, IPR006210; EGF.
 DR InterPro, IPR000742; EGF_3.
 DR InterPro, IPR006209; EGF_like.
 DR InterPro, IPR013032; EGF_like_reg.
 DR InterPro, IPR009003; Pept_Ser_Cys.
 DR InterPro, IPR001254; Peptidase_S1.
 DR InterPro, IPR001314; Peptidase_S1A.
 DR InterPro, IPR000436; Sushi_SCR_CCP.
 DR Pfam, PF00431; CUB; 1.
 DR Pfam, PF00008; EGF; 1.
 DR Pfam, PF00084; Sushi; 2.
 DR Pfam, PF00089; Trypsin; 1.
 DR PRINTS, PR00722; CHYMOTRYPSIN.
 DR SMART, SM00032; CCP; 2.
 DR SMART, SM00042; CUB; 1.
 DR SMART, SM00181; EGF; 2.
 DR SMART, SM00020; Tryp_Spc; 1.
 DR PROSITE, PS01180; CUB; 1.
 Query Match 91.6%; Score 3612; DB 2; Length 720;
 Best Local Similarity 90.1%; Pred. No. 4.7e-263;
 Matches 649; Conservative 33; Mismatches 38; Indels 0; Gaps 0;
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 Db 61 VVGTYIPCCNENECDSLIHPGCTIFENCKSCRNSWGGLTDDFYVKGFPYCAECRAGW 120
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 Db 121 YGGDCMKCGVLPARKQIILLESYPLNACBEMTHAKPGVILQRFPMLSLEFDYMQYD 180
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 Db 181 YVEVRDDNDSDPIIRKFCNERNPAPIRSGSSLHVLFHSDGSKNPFDAIYEETPACS 240
 Oy 241 SSPCFHDGTCLVLDKAGSKYKACLAGYTGRCENILLEERNCSDPGCPVNGYQKITGPGLI 300
 Db 241 SSPCFHDGTCLVLDKAGSKYKACLAGYTGRCENILLEERNCSDPGCPVNGYQKITGPGLI 300
 Oy 301 NGRPAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSKQPICTKACBPKISDLVRRVYL 360
 Db 301 NEHRVKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSKQPICTKACBPKISDLVRRVYL 360

QY 361 PMGVSRRETPHOLYSAFAFSKQKLOSAPTKPPALPFGLDPMGYQHLLATLOVEICISPFYR 420
 DB 361 SMGVSRRETPHOLYSAFAFSKQKLOSAPTKPPALPFGLDPMGYQHLLATLOVEICISPFYR 420
 QY 421 RLGSSRRCTLRITKSGRABSCIPICGKIENITAPKTQGLRMPWQAAIYRTSGVADSL 480
 DB 421 RLGSSRRCTLRITKSGRABSCIPICGKIENITAPKTQGLRMPWQAAIYRTSGVADSL 480
 QY 481 HKAMFLVCSGALVNERVTVAACHCTDGLKATMTADLKVLYGFRYRDDDEKTIQS 540
 DB 481 HKAMFLVCSGALVNERVTVAACHCTDGLKATMTADLKVLYGFRYRDDDEKTIQS 540
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 DB 541 LQISATILHPNYDPIILDADIALITLKLDKARISTRVOPICLAASRDISTFQESHITVAG 600
 QY 601 MNVLADVRSPGFNDTLRSGVSVVDSLCEQHEHGHIPVSTYDMMFCASMEPTASPSDI 660
 DB 601 MNVLADVRSPGFNDTLRSGVSVVDSLCEQHEHGHIPVSTYDMMFCASMEPTASPSDI 660
 QY 661 CTRATGCIANAIVSPGASPPRRHMLGLVSWSTDYKTSRHLSTAFKVLFPKQMIERNMK 720
 DB 661 CTRATGCIANAIVSPGASPPRRHMLGLVSWSTDYKTSRHLSTAFKVLFPKQMIERNMK 720
 RESULT 9
 QY 08K2B8_MOUSE PRELIMINARY; PRT; 720 AA.
 AC 08K2B8;
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 18-APR-2006, entry version 25.
 DE Regeneration associated muscle protease.
 GN Name=E3430002G05R1K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CZECH II; TISSUE=Mammary tumor metastasized to lung. Tumor
 RC arose spontaneously;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Deje J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uadiri T.B., Yoshizaki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=CZECH II; TISSUE=Mammary tumor metastasized to lung. Tumor
 RC arose spontaneously;
 RA Strausberg R.,
 RN Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=CZECH II; TISSUE=Mammary tumor metastasized to lung. Tumor

RC arose spontaneously;
 RA Director MGC Project;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
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 DR EMBL: BC031841.1; AAH31841.1; -; mRNA.
 DR EMBL: BC057685; AAH57685.1; -; mRNA.
 DR UniGene: Mm.28649; -.
 DR HSSP: P00736; 1GPE.
 DR MEROPS: S01.998; -.
 DR Ensembl: ENSMUSG00000027188; Mus musculus.
 DR MGI: MGI:2445082; E3430002G05R1K.
 DR GO: GO:0005615; Cytochrome c; extracellular space; RCA.
 DR GO: GO:0004263; F1-ATPase activity; RCA.
 DR GO: GO:0004295; F1-ATPase activity; RCA.
 DR GO: GO:0005508; P-protein synthesis; RCA.
 DR InterPro: IPR000659; CUB.
 DR InterPro: IPR006210; EGF.
 DR InterPro: IPR000742; EGF.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR013032; EGF-like reg.
 DR InterPro: IPR009003; Pept Ser Cys.
 DR InterPro: IPR001254; Peptidase_S1_S6.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00431; CUB; 1.
 DR Pfam: PF00008; EGF; 1.
 DR Pfam: PF00084; Sushi; 2.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR SMART: SM00032; CCP; 2.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00020; Tryp_Spc; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS00022; EGF; 1.
 DR PROSITE: PS01186; EGF; 2; 1.
 DR PROSITE: PS50026; EGF; 3; 1.
 DR PROSITE: PS50923; SUSHI; 2.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 KM Protease.
 SQ SEQUENCE 720 AA; 80378 MW; 7172B7F1E690ED0E CRC64;
 Query Match 91.6%; Score 3612; DB 2; Length 720;
 Best Local Similarity 90.1%; Pred. No. 4,7e-263;
 Matches 649; Conservative 33; Mismatches 38; Indels 0; Gaps 0;
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 DB 1 MEIDRWAQGLVFLQLLISSPREYTVINEACPGAEWIMCRCECYDQICVCPGRK 60
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 DB 61 VVGCTTPCCRNENEDSCILHPGCTIFENKSCRGSGGLDPEYVGVFCCEERACW 120
 QY 121 YGGDCRCQGVLRAPKQILLISYPANAHCETTHAKPQVLRVMLSLFEDVYCYD 180
 DB 121 YGGDCRCQGVLRAPKQILLISYPANAHCETTHAKPQVLRVMLSLFEDVYCYD 180
 QY 181 YVEVRDGNDRDQIIRKVCNERNPAPISGSSLHVLHFSDSKNDGFAHYEITACS 240
 DB 181 YVEVRDGNDRDQIIRKVCNERNPAPISGSSLHVLHFSDSKNDGFAHYEITACS 240
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 DB 241 SSPCFHDGTCVLDKXGSYCACLAGYTGRCENLLEERNCSPPGCVNYSOKITGPGIL 300
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 DB 301 NGRHAKIGTVVAFCCNNSYVLSGNEKRTCOQNGMSGKOPICAKCREPKISDLVRRYL 360


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Db      601  SGRKLLSDPRAPSPKMETIAGALIEPVDLSQCEQVBEENGISVSYESMFCAGQERPRSP 660
QY      659  DICTAETGCIAAVSPFGRAPEPRMHLMLGLVMSYDKTCSHRLSTAFKVLPRKDWIERN 718
Db      661  SICPSEGTITVLTPSPSPSGEWHLIGVSWGDKSCRKDLTYGTAKVTEKWELEKN 720
QY      719  MK 720
Db      721  MK 722

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RESULT 11

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Q71R89 HUMAN PRELIMINARY; PRT; 417 AA.
ID 071R89 HUMAN PRELIMINARY; PRT; 417 AA.
AC 071R89;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 18-APR-2006, entry version 12.
DE P938.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Hominoidea; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the peptidase S1 family.
CC -----
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CC -----
DR EMBL; AF370388; AAQ15224.1; -; mRNA.
DR HSSP; P00734; 1BB0.
DR Ensembl; ENSG00000149090; Homo sapiens.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00084; Sush1; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYSPC; 1.
DR PROSITE; PS00923; SUSH1; 1.
DR PROSITE; PS02440; TRYPSIN_DOM; 1.
DR Serine protease homolog; Sush1.
SQ SEQUENCE 417 AA; 46703 MW; 2546A52A3697C1C4 CRC64;

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Query Match 52.2%; Score 2059; DB 2; Length 417;

Best Local Similarity 95.6%; Pred. No. 2.4e-146; Matches 389; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

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QY      314  FCNNSYVLSCNEKRTCCQNGSEMGKOPICIKACREPKISDLVRRVLPVMOVSRRTPLHQ 373
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QY      374  LYSAAASKKQLQSAFPTKPPALPFGDDLPVNGVQHLTQIQICISPPFRRLGSSRRTCIRTG 433
Db      71  LYSAAASKKQLQSAFPTKPPALPFGDDLPVNGVQHLTQIQICISPPFRRLGSSRRTCIRTG 130
QY      434  KMSGRAASPCIPICGKIENITAPKTQGLRMPQQAIAIYRTSGVDSLHKAMFLVCSGAL 493
Db      131  KMSGRAASPCIPICGKIENITAPKTQGLRMPQQAIAIYRTSGVDSLHKAMFLVCSGAL 190
QY      494  VNERVVVAACHVTDLGKVTMKTADLKVVLGKFRYDDDRDEKTIQSLQISAIILHNVD 553
Db      191  VNERVVVAACHVTDLGKVTMKTADLKVVLGKFRYDDDRDEKTIQSLQISAIILHNVD 250

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QY      554  PILLDADIALKLKLDKARISTVOPICLAASRDISTSPQESHITVAGNVLADVRSRGRK 613
Db      251  PILLDADIALKLKLDKARISTVOPICLAASRDISTSPQESHITVAGNVLADVRSRGRK 310
QY      614  NDLRSQVSVVDSLLCEQHEHDHGIPVSVTNMFCASNEPTAPSDICTAETGIAAVSF 673
Db      311  NDLRSQVSVVDSLLCEQHEHDHGIPVSVTNMFCASNEPTAPSDICTAETGIAAVSF 370
QY      674  PGRASPEPRMHLMLGLVMSYDKTCSHRLSTAFKVLPRKDWIERNMK 720
Db      371  PGRASPEPRMHLMLGLVMSYDKTCSHRLSTAFKVLPRKDWIERNMK 417

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RESULT 12

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ID 04SAF4 TETNG PRELIMINARY; PRT; 1009 AA.
AC 04SAF4;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 02-MAY-2006, entry version 7.
DE Chromosome 13 SCAR1468, whole genome shotgun sequence.
GN ORFNames=GSTENG00021480001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OC NCBI_Taxid=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozou-Costaz C., Bernot A.,
RA Nicard S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Sainoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Crotolico L., Poulain J., De Bernardinis V.,
RA Cruaud C., Duprat S., Broctier P., Coutanceau J.-P., Guzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
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DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR013032; EGF_1like_reg.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
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DR PRINTS; PR00722; CHYMOTRYPSIN.

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SQ SEQUENCE 1019 AA; 112249 MW; B8E51730AE595993 CRC64;

Search completed: April 4, 2007, 22:04:11
Job time : 399 secs

Query Match 17.2%; Score 678; DB 2; Length 1019;
Best Local Similarity 25.6%; Pred. No. 8.5e-42;
Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;

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GenCore version 6.2
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OM protein - protein search, using sw model

Run on: April 4, 2007, 21:55:04 ; Search time 30 Seconds

(without alignments)
2100.735 Million cell updates/sec

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Perfect score: 3945

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Scoring table: BLOSUM62

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	3945	100.0	720	2	US-09-997-333-231
4	3945	100.0	720	2	US-09-992-598-231
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6	3945	100.0	720	3	US-09-989-726-231
7	3945	100.0	720	3	US-09-997-514-231
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154	275.5	7.0	406	5	PCT-US92-10242-5	Sequence 5, Appl	227	248	6.3	231	3	US-09-421-213-6	Sequence 6, Appl
155	275.5	7.0	444	1	US-08-475-845-2	Sequence 2, Appl	228	248	6.3	638	2	US-10-099-322-111	Sequence 111, App
156	275.5	7.0	444	1	US-08-327-690-2	Sequence 2, Appl	229	247	6.3	638	2	US-10-044-564-111	Sequence 111, App
157	275.5	7.0	444	1	US-08-660-289-2	Sequence 2, Appl	230	247	6.3	638	2	US-10-099-322-30	Sequence 30, Appl
158	275.5	7.0	444	1	US-08-537-807-2	Sequence 2, Appl	231	247	6.3	638	2	US-10-044-564-30	Sequence 30, Appl
159	275.5	7.0	444	1	US-08-871-003-2	Sequence 2, Appl	232	247	6.3	764	1	US-08-177-109A-2	Sequence 2, Appl
160	275.5	7.0	444	2	US-08-464-233-2	Sequence 2, Appl	233	247	6.3	764	1	US-08-687-706-2	Sequence 2, Appl
161	275.5	7.0	444	2	US-09-189-607-2	Sequence 2, Appl	234	247	6.3	764	2	US-09-949-002-325	Sequence 325, App
162	275.5	7.0	444	2	US-09-378-907-2	Sequence 2, Appl	235	247	6.3	768	2	US-09-949-016-11021	Sequence 11021, A
163	275.5	7.0	444	5	PCT-US94-05779-2	Sequence 2, Appl	236	247	6.3	798	2	US-09-949-002-544	Sequence 544, App
164	275.5	7.0	461	2	US-09-949-016-8839	Sequence 8839, App	237	247	6.3	986	2	US-09-949-016-6690	Sequence 6690, App
165	275	7.0	562	7	5244676-5	Sequence 4676-5	238	246.5	6.2	259	2	US-08-944-483-52	Sequence 52, Appl
166	275	7.0	1113	2	US-09-949-016-6458	Sequence 6458, Ap	239	246.5	6.2	376	2	US-08-338-368-2	Sequence 2, Appl
167	273	6.9	560	2	US-09-912-559-3	Sequence 3, Appl	240	246.5	6.2	376	2	US-08-558-869-10	Sequence 10, Appl
168	273	6.9	560	2	US-09-912-559-4	Sequence 4, Appl	241	246.5	6.2	376	2	US-09-410-882-10	Sequence 10, Appl
169	273	6.9	560	2	US-08-487-037-1	Sequence 1, Appl	242	246.5	6.2	579	1	US-08-295-411-4	Sequence 4, Appl
170	272	6.9	488	1	US-09-856-050-15	Sequence 15, Appl	243	246.5	6.2	579	1	US-08-955-471-4	Sequence 4, Appl
171	271.5	6.9	223	3	US-08-361-395-1	Sequence 1, Appl	244	246.5	6.2	579	2	US-09-117-708-14	Sequence 14, Appl
172	271.5	6.9	244	1	US-08-361-395-1	Sequence 1, Appl	245	246.5	6.2	579	5	PCT-US92-10242-4	Sequence 4, Appl

246	246.5	6.2	615	1	US-07-998-972A-3	Sequence 3, Appl1	319	236.5	6.0	416	2	US-10-099-323-138	Sequence 138, App
247	246.5	6.2	615	1	US-08-463-953-3	Sequence 3, Appl1	320	236.5	6.0	416	2	US-10-044-564-138	Sequence 138, App
248	246.5	6.2	615	1	US-08-462-261-3	Sequence 3, Appl1	321	236.5	6.0	416	2	US-08-811-949-63	Sequence 63, Appl
249	246.5	6.2	615	5	PCT-US92-11357-3	Sequence 3, Appl1	322	236.5	6.0	871	2	US-09-245-041-19	Sequence 19, Appl
250	246.5	6.2	622	2	US-08-952-967-8	Sequence 42, Appl1	323	236.5	6.0	871	2	US-09-358-055B-19	Sequence 19, Appl
251	246.5	6.2	622	2	US-09-054-272-42	Sequence 42, Appl1	324	236.5	6.0	871	2	US-09-893-238-19	Sequence 19, Appl
252	246.5	6.2	812	2	US-08-991-761A-7	Sequence 7, Appl1	325	236.5	6.0	1013	1	US-08-866-600-8	Sequence 3, Appl1
253	245.5	6.2	638	2	US-10-099-322-112	Sequence 112, App	326	236.5	6.0	1013	1	US-08-866-600-8	Sequence 3, Appl1
254	245.5	6.2	638	2	US-10-044-564-112	Sequence 112, App	327	236.5	6.0	1013	2	US-09-021-287-3	Sequence 3, Appl1
255	245	6.2	228	1	US-08-278-091-10	Sequence 10, Appl	328	236.5	6.0	1013	2	US-09-240-473-3	Sequence 3, Appl1
256	245	6.2	228	1	US-08-483-859-10	Sequence 10, Appl	329	236.5	6.0	1350	2	US-09-358-055B-17	Sequence 17, Appl
257	245	6.2	228	1	US-08-472-173-10	Sequence 10, Appl	330	236.5	6.0	1350	2	US-09-893-238-17	Sequence 17, Appl
258	245	6.2	228	1	US-08-487-167-10	Sequence 10, Appl	331	236	6.0	355	1	US-08-811-949-53	Sequence 53, Appl
259	245	6.2	228	1	US-08-482-816-10	Sequence 10, Appl	332	236	6.0	355	1	US-08-811-949-59	Sequence 59, Appl
260	245	6.2	228	1	US-08-296-149-10	Sequence 10, Appl	333	235	6.0	270	1	US-08-978-404B-8	Sequence 8, Appl1
261	245	6.2	228	1	US-08-801-499-10	Sequence 10, Appl	334	233.5	5.9	252	2	US-08-944-483-72	Sequence 72, Appl
262	245	6.2	228	1	US-08-615-271-10	Sequence 10, Appl	335	233.5	5.9	253	1	US-09-027-337-8	Sequence 8, Appl1
263	245	6.2	228	2	US-09-074-660-10	Sequence 10, Appl	336	233.5	5.9	253	2	US-09-644-600-8	Sequence 8, Appl1
264	245	6.2	228	2	US-09-106-468-10	Sequence 10, Appl	337	233.5	5.9	253	2	US-09-654-600A-8	Sequence 8, Appl1
265	245	6.2	228	2	US-09-106-468-10	Sequence 10, Appl	338	233.5	5.9	253	3	US-09-421-213-8	Sequence 8, Appl1
266	245	6.2	228	2	US-09-106-468-10	Sequence 10, Appl	339	233.5	5.9	268	2	US-09-987-455A-18	Sequence 18, Appl
267	245	6.2	228	2	US-09-106-467-10	Sequence 10, Appl	340	233.5	5.9	383	1	US-08-558-269-6	Sequence 6, Appl1
268	245	6.2	445	2	US-10-360-101-266	Sequence 266, App	341	233.5	5.9	383	2	US-09-410-882-6	Sequence 6, Appl1
269	244.5	6.2	259	2	US-09-715-994-2	Sequence 2, Appl1	342	233.5	5.9	546	7	5200340-6	Patent No. 5200340
270	244	6.2	638	2	US-10-099-322-114	Sequence 114, App	343	232.5	5.9	259	2	US-10-165-442-2	Sequence 2, Appl1
271	244	6.2	638	2	US-10-044-564-114	Sequence 114, App	344	232.5	5.9	295	2	US-10-165-442-1	Sequence 1, Appl1
272	242.5	6.1	436	1	US-09-000-846-2	Sequence 2, Appl1	345	232.5	5.9	1013	1	US-08-866-650-5	Sequence 5, Appl1
273	242	6.1	322	3	US-10-114-270-134	Sequence 134, App	346	232.5	5.9	1013	1	US-09-021-287-5	Sequence 5, Appl1
274	242	6.1	730	2	US-08-872-757-2	Sequence 2, Appl1	347	232.5	5.9	1013	2	US-08-991-408-2	Sequence 2, Appl1
275	242	6.1	730	2	US-09-850-048A-2	Sequence 2, Appl1	348	232.5	5.9	1013	2	US-09-240-473-5	Sequence 5, Appl1
276	241.5	6.1	347	1	US-08-811-949-1	Sequence 1, Appl1	349	232.5	5.9	1013	2	US-09-432-473-2	Sequence 2, Appl1
277	241.5	6.1	788	1	US-08-572-225-1	Sequence 1, Appl1	350	232.5	5.9	1013	2	US-09-285-385C-20	Sequence 20, Appl
278	241	6.1	354	1	US-08-811-949-61	Sequence 61, Appl	351	232	5.9	416	2	US-10-099-322-137	Sequence 137, App
279	241	6.1	966	2	US-08-872-757-4	Sequence 4, Appl1	352	232	5.9	416	2	US-10-044-564-137	Sequence 137, App
280	241	6.1	966	2	US-09-850-048A-4	Sequence 4, Appl1	353	232	5.9	638	2	US-08-681-151-3	Sequence 3, Appl1
281	240.5	6.1	356	1	US-08-427-640-8	Sequence 8, Appl1	354	232	5.9	638	2	US-10-099-322-115	Sequence 115, App
282	240.5	6.1	3571	2	US-09-911-842A-2	Sequence 2, Appl1	355	232	5.9	638	2	US-10-044-564-115	Sequence 115, App
283	240	6.1	432	2	US-09-959-392-34	Sequence 34, Appl	356	231.5	5.9	389	1	US-08-811-949-65	Sequence 65, Appl
284	240	6.1	432	2	US-08-560-098A-47	Sequence 47, Appl	357	231.5	5.9	417	2	US-09-820-002-4	Sequence 4, Appl1
285	239.5	6.1	1015	2	US-09-285-385C-2	Sequence 2, Appl1	358	231	5.9	365	1	US-08-093-741-83	Sequence 83, Appl
286	239.5	6.1	3594	4	US-09-911-842A-4	Sequence 4, Appl1	359	231	5.9	365	1	US-08-720-012-83	Sequence 83, Appl
287	239	6.1	230	2	US-09-601-318-3	Sequence 3, Appl1	360	231	5.9	393	1	US-08-560-098A-44	Sequence 44, Appl
288	239	6.1	356	1	US-08-681-151-1	Sequence 1, Appl1	361	231	5.9	393	2	US-08-967-024C-24	Sequence 24, Appl
289	239	6.1	389	1	US-08-811-949-67	Sequence 67, Appl	362	231	5.9	393	2	US-08-967-024C-25	Sequence 25, Appl
290	238.5	6.0	437	1	US-08-811-949-49	Sequence 49, Appl	363	231	5.9	1012	2	US-09-285-385C-4	Sequence 4, Appl1
291	238.5	6.0	437	1	US-08-811-949-51	Sequence 51, Appl	364	230.5	5.8	259	2	US-10-165-442-4	Sequence 4, Appl1
292	238.5	6.0	437	1	US-08-811-949-55	Sequence 55, Appl	365	230.5	5.8	295	2	US-10-165-442-4	Sequence 4, Appl1
293	238.5	6.0	437	1	US-08-811-949-57	Sequence 57, Appl	366	230.5	5.8	302	2	US-09-220-731-26	Sequence 26, Appl
294	238	6.0	237	2	US-08-163-919A-3	Sequence 3, Appl1	367	230.5	5.8	302	2	US-09-242-999-22	Sequence 22, Appl
295	238	6.0	237	2	US-08-462-515-3	Sequence 3, Appl1	368	230	5.8	232	2	US-09-959-392-31	Sequence 31, Appl
296	238	6.0	237	5	PCT-US94-14073-3	Sequence 3, Appl1	369	230	5.8	248	2	US-08-944-483-63	Sequence 63, Appl
297	238	6.0	335	2	US-09-987-455A-14	Sequence 14, Appl	370	230	5.8	387	2	US-09-032-215-8	Sequence 8, Appl1
298	238	6.0	274	1	US-09-987-455A-16	Sequence 16, Appl	371	230	5.8	387	2	US-09-032-215-13	Sequence 13, Appl
299	236.5	6.0	308	2	US-08-987-455A-17	Sequence 17, Appl	372	229	5.8	242	2	US-09-004-721-36	Sequence 36, Appl
300	236.5	6.0	331	2	US-09-987-455A-12	Sequence 12, Appl	373	229	5.8	242	2	US-08-749-699-36	Sequence 36, Appl
301	236.5	6.0	339	2	US-09-987-455A-13	Sequence 13, Appl	374	229	5.8	242	2	US-09-004-729-36	Sequence 36, Appl
302	236.5	6.0	339	2	US-09-987-455A-13	Sequence 13, Appl	375	229	5.8	400	2	US-09-004-729-36	Sequence 36, Appl
303	236.5	6.0	334	2	US-09-987-455A-11	Sequence 11, Appl	376	229	5.8	400	2	US-09-004-731-33	Sequence 33, Appl
304	236.5	6.0	334	2	US-09-987-455A-11	Sequence 11, Appl	377	229	5.8	400	2	US-08-749-699-30	Sequence 30, Appl
305	236.5	6.0	335	1	US-08-137-116-1	Sequence 1, Appl1	378	229	5.8	400	2	US-08-749-699-33	Sequence 33, Appl
306	236.5	6.0	335	1	US-08-217-618-1	Sequence 1, Appl1	379	229	5.8	400	2	US-09-004-729-30	Sequence 30, Appl
307	236.5	6.0	335	1	US-08-427-640-2	Sequence 2, Appl1	380	229	5.8	400	2	US-09-004-729-33	Sequence 33, Appl
308	236.5	6.0	335	1	US-08-427-640-6	Sequence 6, Appl1	381	228.5	5.8	235	2	US-09-004-729-33	Sequence 33, Appl
309	236.5	6.0	335	1	US-08-217-617A-1	Sequence 1, Appl1	382	228.5	5.8	235	2	US-08-807-151-3	Sequence 3, Appl1
310	236.5	6.0	335	1	US-08-217-617A-1	Sequence 1, Appl1	383	228.5	5.8	343	3	US-10-162-335-86	Sequence 86, Appl
311	236.5	6.0	335	1	US-08-811-949-45	Sequence 45, Appl	384	228	5.8	287	3	US-10-114-270-130	Sequence 130, App
312	236.5	6.0	335	2	US-08-811-949-47	Sequence 47, Appl	385	228	5.8	591	2	US-08-991-408-4	Sequence 4, Appl1
313	236.5	6.0	335	2	US-08-794-528-1	Sequence 47, Appl	386	228	5.8	591	2	US-09-432-473-4	Sequence 4, Appl1
314	236.5	6.0	335	7	5223256-1	Patent No. 5223256	387	228	5.8	809	2	US-08-991-761A-9	Sequence 9, Appl1
315	236.5	6.0	336	1	US-08-427-640-4	Sequence 4, Appl1	388	228	5.8	812	1	US-08-451-932-1	Sequence 1, Appl1
316	236.5	6.0	377	2	US-09-987-455A-8	Sequence 8, Appl1	389	228	5.8	812	1	US-08-451-932-1	Sequence 1, Appl1
317	236.5	6.0	378	2	US-09-553-498-10	Sequence 10, Appl	390	228	5.8	812	1	US-08-452-260-1	Sequence 1, Appl1
318	236.5	6.0	378	2	US-09-618-869-10	Sequence 10, Appl	391	228	5.8	812	1	US-08-326-785-1	Sequence 1, Appl1

392	228	5.8	812	1	US-08-612-788-1	Sequence 1, Appl1	465	223	5.7	521	2	US-09-949-016-11081	Sequence 11081, A
393	228	5.8	812	1	US-08-605-598B-1	Sequence 1, Appl1	466	223	5.7	521	2	US-09-949-016-11082	Sequence 11082, A
394	228	5.8	812	1	US-08-429-743-1	Sequence 1, Appl1	467	223	5.7	521	2	US-09-949-016-11083	Sequence 11083, A
395	228	5.8	812	1	US-08-866-735-1	Sequence 1, Appl1	468	222.5	5.6	304	2	US-10-039-322-139	Sequence 139, App
396	228	5.8	812	2	US-09-066-028-1	Sequence 1, Appl1	469	222.5	5.6	304	2	US-10-044-564-139	Sequence 139, App
397	228	5.8	812	2	US-09-192-012-3	Sequence 3, Appl1	470	222.5	5.6	380	2	US-10-235-789C-2	Sequence 2, Appl1
398	228	5.8	812	2	US-09-335-325-1	Sequence 1, Appl1	471	222.5	5.6	417	2	US-10-099-122-40	Sequence 40, Appl1
399	228	5.8	812	2	US-08-991-761A-12	Sequence 12, Appl1	472	222.5	5.6	417	2	US-10-099-122-136	Sequence 136, App
400	228	5.8	812	2	US-09-335-614-1	Sequence 1, Appl1	473	222.5	5.6	417	2	US-10-044-564-136	Sequence 40, Appl1
401	228	5.8	812	5	PCT-US95-05107-1	Sequence 1, Appl1	474	222.5	5.6	417	2	US-10-044-564-136	Sequence 136, App
402	237.5	5.8	237	3	US-09-936-271C-66	Sequence 66, Appl1	475	222.5	5.6	445	2	US-09-856-771A-8	Sequence 8, Appl1
403	227.5	5.8	251	3	US-09-936-271C-67	Sequence 67, Appl1	476	222.5	5.6	452	2	US-09-949-016-7182	Sequence 7182, Ap
404	227	5.8	241	3	US-09-657-986B-2	Sequence 2, Appl1	477	222.5	5.6	790	2	US-08-991-761A-13	Sequence 13, Appl1
405	227	5.8	241	3	US-09-410-362F-3	Sequence 3, Appl1	478	222	5.6	224	1	US-09-016-1666A-21	Sequence 21, Appl1
406	227	5.8	241	3	US-09-410-362F-35	Sequence 35, Appl1	479	222	5.6	224	1	US-08-978-004B-16	Sequence 16, Appl1
407	227	5.8	308	2	US-09-023-942A-26	Sequence 26, Appl1	480	222	5.6	407	2	US-09-734-675-4	Sequence 4, Appl1
408	227	5.8	308	2	US-08-705-875A-10	Sequence 10, Appl1	481	222	5.6	407	2	US-10-060-333-4	Sequence 4, Appl1
409	227	5.8	308	2	US-09-242-999-10	Sequence 10, Appl1	482	222	5.6	433	2	US-10-012-231A-269	Sequence 269, App
410	226.5	5.7	454	2	US-09-518-046-2	Sequence 2, Appl1	483	222	5.6	433	2	US-10-015-189A-269	Sequence 269, App
411	226.5	5.7	454	2	US-09-650-371-2	Sequence 2, Appl1	484	222	5.6	433	2	US-10-006-768A-269	Sequence 269, App
412	226.5	5.7	2787	2	US-09-245-041-15	Sequence 15, Appl1	485	222	5.6	433	2	US-10-015-671A-269	Sequence 269, App
413	226.5	5.7	2787	2	US-09-358-055B-15	Sequence 15, Appl1	486	222	5.6	433	2	US-10-015-393A-269	Sequence 269, App
414	226.5	5.7	2787	2	US-09-893-238-15	Sequence 15, Appl1	487	222	5.6	433	2	US-10-011-833A-269	Sequence 269, App
415	226	5.7	406	2	US-09-851-588-6	Sequence 6, Appl1	488	222	5.6	433	2	US-10-006-041A-269	Sequence 269, App
416	226	5.7	423	2	US-09-656-002-2	Sequence 2, Appl1	489	222	5.6	433	2	US-10-012-064A-269	Sequence 269, App
417	226	5.7	432	2	US-10-012-211A-275	Sequence 275, App	490	222	5.6	433	2	US-10-015-392A-269	Sequence 269, App
418	226	5.7	432	2	US-10-015-389A-275	Sequence 275, App	491	222	5.6	433	3	US-10-011-795B-269	Sequence 269, App
419	226	5.7	432	2	US-10-006-768A-275	Sequence 275, App	492	222	5.6	433	3	US-10-015-386A-269	Sequence 269, App
420	226	5.7	432	2	US-10-006-768A-275	Sequence 275, App	493	222	5.6	433	3	US-10-012-121A-269	Sequence 269, App
421	226	5.7	432	2	US-10-015-671A-275	Sequence 275, App	494	222	5.6	433	3	US-10-006-485A-269	Sequence 269, App
422	226	5.7	432	2	US-10-015-333A-275	Sequence 275, App	495	222	5.6	433	3	US-10-006-485A-269	Sequence 269, App
423	226	5.7	432	2	US-10-011-833A-275	Sequence 275, App	496	222	5.6	433	3	US-10-006-485A-269	Sequence 269, App
424	226	5.7	432	2	US-10-006-041A-275	Sequence 275, App	497	222	5.6	433	3	US-10-012-752A-275	Sequence 275, App
425	226	5.7	432	2	US-10-012-064A-275	Sequence 275, App	498	222	5.6	433	3	US-10-017-523A-269	Sequence 269, App
426	226	5.7	432	3	US-10-015-392A-275	Sequence 275, App	499	222	5.6	433	3	US-10-015-519A-269	Sequence 269, App
427	226	5.7	432	3	US-10-011-795B-275	Sequence 275, App	500	222	5.6	433	3	US-10-015-519A-269	Sequence 269, App
428	226	5.7	432	3	US-10-015-386A-275	Sequence 275, App	501	221.5	5.6	433	3	US-10-007-636A-269	Sequence 269, App
429	226	5.7	432	3	US-10-012-121A-275	Sequence 275, App	502	221.5	5.6	433	3	US-09-999-873A-69	Sequence 69, App
430	226	5.7	432	3	US-10-006-485A-275	Sequence 275, App	503	221.5	5.6	433	2	US-10-020-045A-69	Sequence 69, App
431	226	5.7	432	3	US-10-006-746A-275	Sequence 275, App	504	221.5	5.6	433	2	US-09-978-189-69	Sequence 69, App
432	226	5.7	432	3	US-10-012-752A-275	Sequence 275, App	505	221.5	5.6	433	2	US-10-017-085A-69	Sequence 69, App
433	226	5.7	432	3	US-10-017-253A-275	Sequence 275, App	506	221.5	5.6	433	3	US-10-145-129A-69	Sequence 69, App
434	226	5.7	432	3	US-10-015-519A-275	Sequence 275, App	507	221.5	5.6	433	3	US-10-013-929A-69	Sequence 69, App
435	226	5.7	432	3	US-10-015-715A-275	Sequence 275, App	508	221.5	5.6	253	3	US-10-013-917A-69	Sequence 69, App
436	226	5.7	435	2	US-10-007-236A-275	Sequence 275, App	509	221	5.6	253	3	US-08-944-483-73	Sequence 73, Appl1
437	226	5.7	435	2	US-09-608-271A-6	Sequence 6, Appl1	510	221	5.6	253	1	US-08-978-404B-6	Sequence 6, Appl1
438	226	5.7	435	2	US-09-607-745-2	Sequence 6, Appl1	511	221	5.6	300	2	US-08-705-875A-6	Sequence 6, Appl1
439	226	5.7	435	2	US-09-968-415-6	Sequence 6, Appl1	512	221	5.6	1153	2	US-09-242-999-6	Sequence 6, Appl1
440	226	5.7	437	3	US-10-030-688-2	Sequence 2, Appl1	513	221	5.6	1153	2	US-09-949-016-10498	Sequence 10498, A
441	226	5.7	437	3	US-09-851-588-8	Sequence 8, Appl1	514	220.5	5.6	1355	2	US-09-787-097-17	Sequence 10, Appl1
442	226	5.7	481	2	US-09-949-016-9238	Sequence 9238, Ap	515	220	5.6	273	1	US-09-820-002-2	Sequence 2, Appl1
443	226	5.7	492	3	US-09-949-016-9239	Sequence 9239, Ap	516	220	5.6	273	1	US-09-016-366A-19	Sequence 19, Appl1
444	226	5.7	637	2	US-10-030-688-4	Sequence 4, Appl1	517	219.5	5.6	273	1	US-08-978-404B-14	Sequence 14, Appl1
445	226	5.7	637	2	US-09-949-016-11538	Sequence 11538, A	518	219.5	5.6	245	3	US-09-410-362F-36	Sequence 36, Appl1
446	225.5	5.7	637	2	US-09-949-016-11539	Sequence 11539, A	519	219.5	5.6	245	3	US-09-410-362F-36	Sequence 36, Appl1
447	225.5	5.7	457	2	US-09-949-016-5979	Sequence 6979, Ap	520	219.5	5.6	255	1	US-09-027-37-7	Sequence 7, Appl1
448	225.5	5.7	1272	2	US-09-856-371A-10	Sequence 10, Appl1	521	219.5	5.6	255	2	US-09-644-600-7	Sequence 7, Appl1
449	225.5	5.7	1429	2	US-09-787-097-18	Sequence 18, Appl1	522	219.5	5.6	255	2	US-09-654-600A-7	Sequence 7, Appl1
450	225	5.7	615	2	US-09-787-097-12	Sequence 12, Appl1	523	219	5.6	255	3	US-09-654-600A-7	Sequence 7, Appl1
451	224.5	5.7	615	2	US-09-949-002-001	Sequence 301, App	524	219	5.6	255	3	US-09-421-213-7	Sequence 7, Appl1
452	224.5	5.7	232	2	US-09-959-392-32	Sequence 32, Appl1	525	218.5	5.5	333	2	US-09-948-094-2	Sequence 2, Appl1
453	224.5	5.7	235	2	US-08-944-483-65	Sequence 65, Appl1	526	218.5	5.5	244	2	US-10-037-617-130	Sequence 130, App
454	224.5	5.7	235	3	US-09-410-362F-5	Sequence 5, Appl1	527	218.5	5.5	244	2	US-09-601-318-5	Sequence 5, Appl1
455	224	5.7	275	1	US-09-410-362F-37	Sequence 37, Appl1	528	218.5	5.5	244	2	US-09-601-318-6	Sequence 6, Appl1
456	224	5.7	275	1	US-09-016-366A-17	Sequence 17, Appl1	529	218.5	5.5	245	2	US-09-601-318-7	Sequence 7, Appl1
457	224	5.7	275	1	US-08-978-404B-12	Sequence 12, Appl1	530	218.5	5.5	245	2	US-09-079-970A-6	Sequence 6, Appl1
458	224	5.7	276	2	US-09-598-982C-52	Sequence 52, Appl1	531	218.5	5.5	245	2	US-09-601-318-1	Sequence 1, Appl1
459	224	5.7	306	1	US-08-560-098A-45	Sequence 5, Appl1	532	218.5	5.5	245	2	US-09-079-970A-5	Sequence 11, Appl1
460	224	5.7	323	2	US-08-560-098A-45	Sequence 45, Appl1	533	218.5	5.5	249	2	US-09-598-982C-9	Sequence 9, Appl1
461	224	5.7	331	1	US-09-880-503-7	Sequence 7, Appl1	534	217.5	5.5	245	2	US-09-598-982C-33	Sequence 33, Appl1
462	223.5	5.7	323	1	US-08-560-098A-46	Sequence 46, Appl1	535	217.5	5.5	249	2	US-09-598-982C-35	Sequence 35, Appl1
463	223.5	5.7	245	2	US-08-944-483-69	Sequence 69, Appl1	536	217.5	5.5	249	2	US-09-598-982C-25	Sequence 25, Appl1
464	223	5.7	346	2	US-09-949-016-9000	Sequence 9000, Ap	537	217.5	5.5	249	2	US-09-598-982C-27	Sequence 27, Appl1

538	217.5	5.5	1198	2	US-09-245-041-131	Sequence 131, App	611	214	5.4	254	1	US-08-560-098A-49	Sequence 49, Appl
539	217.5	5.5	1198	2	US-09-794-236-3	Sequence 3, Appl	612	214	5.4	292	2	US-09-607-745-9	Sequence 9, Appl
540	217.5	5.5	1198	2	US-09-358-055B-132	Sequence 132, Appl	613	214	5.4	342	2	US-10-037-417-133	Sequence 133, App
541	217.5	5.5	1198	2	US-09-964-956-35	Sequence 35, Appl	614	214	5.4	342	2	US-10-037-417-134	Sequence 134, App
542	217.5	5.5	1198	2	US-09-787-097-2	Sequence 2, Appl	615	213.5	5.4	215	1	US-09-964-956-68	Sequence 68, Appl
543	217.5	5.5	1429	2	US-09-245-041-130	Sequence 130, App	616	213.5	5.4	255	2	US-08-944-483-67	Sequence 67, Appl
544	217.5	5.5	1429	2	US-09-358-055B-131	Sequence 131, App	617	213.5	5.4	255	3	US-09-410-362P-6	Sequence 6, Appl
545	217.5	5.5	1429	2	US-08-944-483-61	Sequence 61, Appl	618	213.5	5.4	255	3	US-09-410-362P-38	Sequence 38, Appl
546	217	5.5	258	2	US-09-613-822B-2	Sequence 2, Appl	619	213.5	5.4	256	1	US-09-027-337-3	Sequence 3, Appl
547	217	5.5	234	2	US-08-978-404B-3	Sequence 4, Appl	620	213.5	5.4	256	2	US-09-644-600A-3	Sequence 3, Appl
548	217	5.5	343	2	US-10-037-417-44	Sequence 46, Appl	621	213.5	5.4	256	2	US-09-654-600A-3	Sequence 3, Appl
549	217	5.5	791	2	US-10-037-417-46	Sequence 1, Appl	622	213.5	5.4	256	2	US-09-421-213-3	Sequence 3, Appl
550	217	5.5	791	2	US-08-643-219-1	Sequence 1, Appl	623	212.5	5.4	250	2	US-09-205-258-427	Sequence 427, App
551	217	5.5	791	2	US-08-851-350-1	Sequence 19, Appl	624	212.5	5.4	250	2	US-10-004-860-427	Sequence 427, App
552	217	5.5	2703	2	US-08-899-332-4	Sequence 4, Appl	625	212.5	5.4	250	2	US-10-012-231A-170	Sequence 170, App
553	217	5.5	2703	2	US-08-899-332-4	Sequence 4, Appl	626	212.5	5.4	250	2	US-10-015-389A-170	Sequence 170, App
554	217	5.5	2703	2	US-09-121-457-4	Sequence 2, Appl	627	212.5	5.4	250	2	US-10-006-768A-170	Sequence 170, App
555	216.5	5.5	245	2	US-09-598-982C-2	Sequence 2, Appl	628	212.5	5.4	250	2	US-10-015-671A-170	Sequence 170, App
556	216.5	5.5	249	2	US-09-598-982C-6	Sequence 6, Appl	629	212.5	5.4	250	2	US-10-015-393A-170	Sequence 170, App
557	216.5	5.5	498	2	US-10-183-992-2	Sequence 23, Appl	630	212.5	5.4	250	2	US-10-011-833A-170	Sequence 170, App
558	216	5.5	257	1	US-09-016-366A-23	Sequence 101, App	631	212.5	5.4	250	2	US-10-006-041A-170	Sequence 170, App
559	216	5.5	257	1	US-08-978-404B-18	Sequence 18, App	632	212.5	5.4	250	2	US-10-012-064A-170	Sequence 170, App
560	216	5.5	267	2	US-09-917-254-101	Sequence 2, Appl	633	212.5	5.4	250	2	US-10-015-392A-170	Sequence 170, App
561	216	5.5	268	1	US-08-568-031-2	Sequence 2, Appl	634	212.5	5.4	250	3	US-10-011-795B-170	Sequence 170, App
562	216	5.5	268	1	US-08-966-319-2	Sequence 2, Appl	635	212.5	5.4	250	3	US-09-936-271C-86	Sequence 86, Appl
563	216	5.5	268	1	US-09-153-304-2	Sequence 6, Appl	636	212.5	5.4	250	3	US-10-015-386A-170	Sequence 170, App
564	216	5.5	299	2	US-08-944-483-66	Sequence 12, Appl	637	212.5	5.4	250	3	US-10-012-121A-170	Sequence 170, App
565	216	5.5	319	2	US-09-386-642-12	Sequence 12, Appl	638	212.5	5.4	250	3	US-10-006-485A-170	Sequence 170, App
566	216	5.5	328	1	US-09-386-642-11	Sequence 54, Appl	639	212.5	5.4	250	3	US-10-012-752A-170	Sequence 170, App
567	216	5.5	790	1	US-08-469-486-54	Sequence 54, Appl	640	212.5	5.4	250	3	US-10-017-253A-170	Sequence 170, App
568	216	5.5	790	1	US-08-469-486-54	Sequence 54, Appl	641	212.5	5.4	250	3	US-10-017-253A-170	Sequence 170, App
569	216	5.5	810	7	5200340-8	Patent No. 5200340	642	212.5	5.4	250	3	US-10-015-519A-170	Sequence 170, App
570	215.5	5.5	245	2	US-09-598-982C-49	Sequence 49, Appl	643	212.5	5.4	250	3	US-10-015-715A-170	Sequence 170, App
571	215.5	5.5	245	2	US-09-598-982C-51	Sequence 51, Appl	644	212.5	5.4	250	3	US-10-015-715A-170	Sequence 170, App
572	215.5	5.5	249	2	US-09-598-982C-41	Sequence 41, Appl	645	212.5	5.4	282	2	US-09-025-059-1	Sequence 1, Appl
573	215.5	5.5	317	2	US-09-598-982C-43	Sequence 43, Appl	646	212.5	5.4	282	2	US-09-856-320A-2	Sequence 2, Appl
574	215.5	5.5	317	2	US-09-386-629-7	Sequence 7, Appl	647	212.5	5.4	289	2	US-09-386-642-14	Sequence 14, Appl
575	215.5	5.5	317	2	US-09-897-794A-263	Sequence 263, App	648	212.5	5.4	289	2	US-10-162-335-4	Sequence 4, Appl
576	215.5	5.5	317	2	US-09-905-125A-263	Sequence 263, App	649	212.5	5.4	289	2	US-10-162-335-8	Sequence 8, Appl
577	215.5	5.5	317	2	US-09-902-775A-263	Sequence 263, App	650	212.5	5.4	289	2	US-09-025-059-3	Sequence 3, Appl
578	215.5	5.5	317	2	US-09-902-775A-263	Sequence 263, App	651	212	5.4	260	2	US-09-618-259-8	Sequence 8, Appl
579	215.5	5.5	317	2	US-09-903-603A-263	Sequence 263, App	652	212	5.4	260	2	US-08-915-659A-10	Sequence 10, Appl
580	215.5	5.5	317	2	US-09-904-920A-263	Sequence 263, App	653	212	5.4	814	1	US-08-750-711-1	Sequence 1, Appl
581	215.5	5.5	317	2	US-09-905-381A-263	Sequence 263, App	654	211.5	5.4	232	1	US-08-508-448B-19	Sequence 19, Appl
582	215.5	5.5	317	2	US-09-909-064-263	Sequence 263, App	655	211.5	5.4	235	1	US-09-410-362P-4	Sequence 4, Appl
583	215.5	5.5	317	2	US-09-906-618-263	Sequence 263, App	656	211.5	5.4	266	3	US-10-162-335-6	Sequence 6, Appl
584	215.5	5.5	317	2	US-10-040-803-7	Sequence 7, Appl	657	211.5	5.4	266	3	US-10-162-335-10	Sequence 10, Appl
585	215.5	5.5	317	2	US-09-906-646-263	Sequence 263, App	658	211.5	5.4	418	1	US-08-508-448C-25	Sequence 25, Appl
586	215.5	5.5	317	2	US-09-904-462-263	Sequence 263, App	659	211.5	5.4	418	2	US-09-370-838-82	Sequence 82, Appl
587	215.5	5.5	317	2	US-09-902-736A-263	Sequence 263, App	660	211.5	5.4	418	2	US-09-370-838-82	Sequence 82, Appl
588	215.5	5.5	317	2	US-09-906-722A-263	Sequence 263, App	661	211.5	5.4	418	2	US-09-854-133-82	Sequence 82, Appl
589	215.5	5.5	317	2	US-09-905-449-263	Sequence 263, App	662	211.5	5.4	418	2	US-09-854-133-82	Sequence 82, Appl
590	215.5	5.5	317	2	US-09-903-562B-263	Sequence 263, App	663	211	5.3	276	1	US-09-016-366A-15	Sequence 15, Appl
591	215.5	5.5	317	2	US-09-906-679A-263	Sequence 263, App	664	211	5.3	276	1	US-08-978-404B-21	Sequence 21, Appl
592	215.5	5.5	317	3	US-09-907-841-263	Sequence 263, App	665	211	5.3	300	2	US-08-705-875A-4	Sequence 4, Appl
593	215.5	5.5	1428	2	US-09-964-956-33	Sequence 33, Appl	666	211	5.3	300	2	US-09-220-731-21	Sequence 21, Appl
594	215	5.4	389	2	US-10-037-417-131	Sequence 131, Appl	667	211	5.3	300	2	US-09-242-999-4	Sequence 4, Appl
595	215	5.4	733	2	US-09-949-016-998B3	Sequence 9983, App	668	211	5.3	300	2	US-09-644-022A-10	Sequence 10, Appl
596	215	5.4	733	2	US-09-657-431A-1	Sequence 1, Appl	669	211	5.3	300	2	US-09-949-016-822A0	Sequence 8220, App
597	215	5.4	791	1	US-09-131-995-1	Sequence 1, Appl	670	211	5.3	1010	2	US-08-882-046-7	Sequence 7, Appl
598	215	5.4	791	1	US-08-832-087B-1	Sequence 1, Appl	671	211	5.3	1010	2	US-09-566-047-7	Sequence 7, Appl
599	215	5.4	791	2	US-08-132-154-1	Sequence 1, Appl	672	211	5.3	1036	2	US-09-068-740A-6	Sequence 6, Appl
600	215	5.4	791	2	US-08-991-761A-6	Sequence 6, Appl	673	211	5.3	1067	2	US-09-579-536C-18	Sequence 18, Appl
601	215	5.4	791	2	US-08-924-287A-1	Sequence 1, Appl	674	211	5.3	1187	2	US-09-068-740A-7	Sequence 7, Appl
602	215	5.4	791	2	US-10-360-101-257	Sequence 257, App	675	211	5.3	1208	2	US-09-199-865-1	Sequence 1, Appl
603	215	5.4	810	2	US-07-854-603-2	Sequence 2, Appl	676	211	5.3	1208	2	US-10-313-329-1	Sequence 1, Appl
604	215	5.4	810	2	US-08-147-000B-29	Sequence 29, Appl	677	211	5.3	1218	1	US-08-400-159-6	Sequence 6, Appl
605	215	5.4	810	2	US-09-086-514-1	Sequence 1, Appl	678	211	5.3	1218	1	US-08-611-729A-6	Sequence 6, Appl
606	215	5.4	810	2	US-09-132-012-5	Sequence 5, Appl	679	211	5.3	1218	2	US-08-882-046-2	Sequence 2, Appl
607	215	5.4	810	2	US-09-403-736-1	Sequence 1, Appl	680	211	5.3	1218	2	US-09-214-278-7	Sequence 7, Appl
608	215	5.4	810	2	US-09-701-265-1	Sequence 1, Appl	681	211	5.3	1218	2	US-09-068-740A-11	Sequence 11, Appl
609	215	5.4	810	3	US-09-946-893C-2	Sequence 2, Appl	682	211	5.3	1218	2	US-09-855-722-7	Sequence 7, Appl
610	214.5	5.4	1428	2	US-09-964-956-34	Sequence 34, Appl	683	211	5.3	1218	2	US-09-566-047-2	Sequence 2, Appl

684	211	5.3	1218	2	US-09-917-254-85	Sequence 85, Appl	757	204.5	5.2	439	2	US-09-949-016-9260	Sequence 9260, Ap
685	211	5.3	1218	2	US-09-195-524-6	Sequence 6, Appl1	758	204	5.2	260	2	US-09-070-526-2	Sequence 2, Appl1
686	211	5.3	1218	2	US-09-579-536C-1	Sequence 1, Appl1	759	204	5.2	260	2	US-09-618-259-7	Sequence 7, Appl1
687	211	5.3	1218	2	US-09-949-016-5902	Sequence 5902, Ap	760	204	5.2	260	2	US-09-999-883A-395	Sequence 395, App
688	211	5.3	1218	2	US-09-310-685-4	Sequence 4, Appl1	761	204	5.2	260	2	US-10-020-445A-335	Sequence 395, App
689	211	5.3	1254	2	US-09-949-016-10297	Sequence 10297, A	762	204	5.2	260	2	US-09-978-189-395	Sequence 395, App
690	210.5	5.3	245	2	US-09-598-982C-31	Sequence 31, Appl	763	204	5.2	260	2	US-10-017-085A-335	Sequence 395, App
691	210.5	5.3	249	2	US-09-598-982C-23	Sequence 23, Appl	764	204	5.2	260	3	US-08-915-659A-7	Sequence 7, Appl1
692	210.5	5.3	418	2	US-09-370-838-62	Sequence 62, Appl	765	204	5.2	260	3	US-10-145-129A-335	Sequence 395, App
693	210.5	5.3	418	2	US-09-854-133-62	Sequence 62, Appl	766	204	5.2	260	3	US-10-013-929A-395	Sequence 395, App
694	210.5	5.3	1219	2	US-08-882-046-5	Sequence 5, Appl1	767	204	5.2	260	3	US-09-936-271C-835	Sequence 83, Appl
695	210.5	5.3	1219	2	US-09-566-047-5	Sequence 5, Appl1	768	204	5.2	260	3	US-10-013-917A-335	Sequence 395, App
696	210	5.3	154	2	US-09-261-416-5	Sequence 5, Appl1	769	203.5	5.2	224	3	US-08-944-483-34	Sequence 34, Appl
697	210	5.3	248	2	US-08-944-483-24	Sequence 24, Appl	770	203.5	5.2	224	3	US-09-410-362F-39	Sequence 39, Appl1
698	210	5.3	446	2	US-10-177-661-4	Sequence 4, Appl1	771	203.5	5.2	224	3	US-09-410-362F-39	Sequence 39, Appl1
699	209.5	5.3	372	3	US-10-162-335-2	Sequence 2, Appl1	772	203.5	5.2	224	3	US-09-949-016-8770	Sequence 8770, Ap
700	209.5	5.3	477	2	US-10-177-661-2	Sequence 2, Appl1	773	203	5.2	363	2	US-09-341-461-2	Sequence 2, Appl1
701	209.5	5.3	562	2	US-09-879-792-12	Sequence 12, Appl1	774	203	5.1	263	2	US-08-807-151-1	Sequence 1, Appl1
702	208.5	5.3	245	2	US-09-598-982C-29	Sequence 29, Appl	775	203	5.1	263	2	US-09-478-957-1	Sequence 1, Appl1
703	208.5	5.3	245	2	US-09-598-982C-47	Sequence 47, Appl	776	202.5	5.1	268	3	US-09-936-271C-73	Sequence 73, Appl
704	208.5	5.3	249	2	US-09-598-982C-21	Sequence 21, Appl	777	202.5	5.1	701	2	US-10-297-895A-19	Sequence 19, Appl
705	208.5	5.3	249	2	US-09-598-982C-39	Sequence 39, Appl	778	202.5	5.1	766	2	US-10-297-895A-21	Sequence 21, Appl
706	208.5	5.3	492	2	US-09-685-166A-895	Sequence 895, App	779	202.5	5.1	927	2	US-10-297-895A-10	Sequence 10, Appl
707	208.5	5.3	492	2	US-09-879-792-14	Sequence 14, Appl	780	202	5.1	2321	2	US-09-230-652-2	Sequence 2, Appl1
708	208.5	5.3	492	2	US-09-679-426-995	Sequence 895, App	781	202	5.1	2321	2	US-09-612-226B-2	Sequence 2, Appl1
709	208.5	5.3	492	2	US-09-759-143-895	Sequence 895, App	782	200.5	5.1	226	2	US-08-584-617-4	Sequence 4, Appl1
710	208.5	5.3	492	2	US-10-012-896-895	Sequence 895, App	783	200.5	5.1	226	2	US-08-378-091-8	Sequence 8, Appl1
711	208.5	5.3	492	3	US-10-144-678A-895	Sequence 895, App	784	200.5	5.1	232	1	US-08-482-816-8	Sequence 8, Appl1
712	208	5.3	238	2	US-09-856-371A-2	Sequence 895, App	785	200.5	5.1	232	1	US-08-482-816-8	Sequence 8, Appl1
713	208	5.3	268	1	US-08-270-564A-2	Sequence 2, Appl1	786	200.5	5.1	232	1	US-08-482-816-8	Sequence 8, Appl1
714	208	5.3	268	1	US-08-765-192-2	Sequence 2, Appl1	787	200.5	5.1	232	1	US-08-482-816-8	Sequence 8, Appl1
715	208	5.3	268	1	US-09-199-793-2	Sequence 2, Appl1	788	200.5	5.1	232	1	US-08-482-816-8	Sequence 8, Appl1
716	208	5.3	271	1	US-08-467-155A-10	Sequence 10, Appl	789	200.5	5.1	232	1	US-08-296-149-8	Sequence 8, Appl1
717	208	5.3	271	1	US-08-628-198-10	Sequence 10, Appl	790	200.5	5.1	232	1	US-08-801-699-8	Sequence 8, Appl1
718	208	5.3	271	2	US-09-201-038-10	Sequence 10, Appl	791	200.5	5.1	232	1	US-08-615-271-8	Sequence 8, Appl1
719	208	5.3	271	2	US-10-021-368-10	Sequence 10, Appl	792	200.5	5.1	232	2	US-09-074-660-8	Sequence 8, Appl1
720	208	5.3	271	5	PCT-US96-079343-10	Sequence 10, Appl	793	200.5	5.1	232	2	US-09-074-660-8	Sequence 8, Appl1
721	208	5.3	273	2	US-09-856-371A-4	Sequence 4, Appl1	794	200.5	5.1	232	2	US-09-106-669-8	Sequence 8, Appl1
722	208	5.3	275	2	US-09-856-320A-6	Sequence 6, Appl1	795	200.5	5.1	232	2	US-09-106-669-8	Sequence 8, Appl1
723	208	5.3	311	2	US-09-856-371A-6	Sequence 6, Appl1	796	200.5	5.1	232	2	US-09-106-669-8	Sequence 8, Appl1
724	207.5	5.3	241	2	US-08-944-483-59	Sequence 59, Appl	797	200.5	5.1	232	1	US-08-956-267A-2	Sequence 2, Appl1
725	206.5	5.2	245	2	US-09-598-982C-45	Sequence 45, Appl	798	200.5	5.1	314	2	US-09-636-882A-2	Sequence 2, Appl1
726	206.5	5.2	249	2	US-09-598-982C-37	Sequence 37, Appl	799	200.5	5.1	415	2	US-09-907-794A-104	Sequence 104, App
727	206.5	5.2	255	1	US-08-650-129-5	Sequence 5, Appl1	800	200.5	5.1	415	2	US-09-905-125A-104	Sequence 104, App
728	206.5	5.2	255	2	US-08-984-417-5	Sequence 5, Appl1	801	200.5	5.1	415	2	US-09-902-775A-104	Sequence 104, App
729	206.5	5.2	284	2	US-09-387-375-7	Sequence 7, Appl1	802	200.5	5.1	415	2	US-09-906-700-104	Sequence 104, App
730	206.5	5.2	284	2	US-10-041-400A-7	Sequence 7, Appl1	803	200.5	5.1	415	2	US-09-903-603A-104	Sequence 104, App
731	206.5	5.2	284	2	US-10-042-091A-7	Sequence 7, Appl1	804	200.5	5.1	415	2	US-09-904-920A-104	Sequence 104, App
732	206.5	5.2	316	2	US-10-041-264B-7	Sequence 7, Appl1	805	200.5	5.1	415	2	US-09-909-664-104	Sequence 104, App
733	206.5	5.2	316	2	US-09-387-375-9	Sequence 9, Appl1	806	200.5	5.1	415	2	US-09-905-581A-104	Sequence 104, App
734	206.5	5.2	316	2	US-10-041-400A-9	Sequence 9, Appl1	807	200.5	5.1	415	2	US-09-906-618-104	Sequence 104, App
735	206.5	5.2	316	2	US-10-042-091A-9	Sequence 9, Appl1	808	200.5	5.1	415	2	US-09-906-646-104	Sequence 104, App
736	206.5	5.2	316	2	US-10-041-264B-9	Sequence 9, Appl1	809	200.5	5.1	415	2	US-09-904-462-104	Sequence 104, App
737	206	5.2	275	3	US-09-936-271C-72	Sequence 72, Appl	810	200.5	5.1	415	2	US-09-902-736A-104	Sequence 104, App
738	206	5.2	1185	2	US-09-964-956-7	Sequence 7, Appl1	811	200.5	5.1	415	2	US-09-906-722A-104	Sequence 104, App
739	205.5	5.2	235	2	US-08-944-483-48	Sequence 48, Appl	812	200.5	5.1	415	2	US-09-905-449-104	Sequence 104, App
740	205.5	5.2	269	1	US-08-978-404B-10	Sequence 10, Appl	813	200.5	5.1	415	2	US-09-903-662B-104	Sequence 104, App
741	205.5	5.2	269	1	US-10-360-101-331	Sequence 231, App	814	200.5	5.1	415	2	US-09-906-679A-104	Sequence 104, App
742	205.5	5.2	288	2	US-09-386-642-13	Sequence 13, Appl	815	200.5	5.1	415	3	US-09-907-841-104	Sequence 104, App
743	205.5	5.2	327	2	US-09-386-629-8	Sequence 8, Appl1	816	200.5	5.1	769	2	US-09-949-016-11019	Sequence 11019, A
744	205.5	5.2	327	2	US-10-040-803-8	Sequence 8, Appl1	817	200.5	5.1	810	2	US-09-964-956-69	Sequence 69, Appl
745	205.5	5.2	360	3	US-10-162-335-14	Sequence 14, Appl	818	200	5.1	110	2	US-09-964-956-69	Sequence 16, Appl
746	205.5	5.2	360	3	US-10-162-335-18	Sequence 18, Appl	819	200	5.1	385	2	US-09-163-951-16	Sequence 16, Appl
747	205.5	5.2	492	2	US-09-342-749-2	Sequence 2, Appl1	820	200	5.1	385	2	US-09-345-881-16	Sequence 16, Appl
748	205.5	5.2	492	2	US-09-691-840-2	Sequence 2, Appl1	821	200	5.1	385	3	US-10-000-512-14	Sequence 14, Appl
749	205.5	5.2	492	2	US-09-759-143-932	Sequence 932, App	822	199.5	5.1	1193	1	US-08-400-159-10	Sequence 10, Appl
750	205.5	5.2	492	2	US-10-012-896-932	Sequence 932, App	823	199.5	5.1	1193	2	US-08-611-729A-10	Sequence 10, Appl
751	205.5	5.2	492	3	US-10-144-678A-932	Sequence 932, App	824	199.5	5.1	1193	2	US-09-195-522A-10	Sequence 10, Appl
752	205.5	5.2	510	2	US-09-949-016-11074	Sequence 11074, A	825	199.5	5.1	1193	2	US-09-310-685-8	Sequence 8, Appl1
753	205	5.2	393	2	US-09-759-143-934	Sequence 934, App	826	199.5	5.1	1275	1	US-09-964-956-36	Sequence 36, Appl
754	205	5.2	393	2	US-10-012-896-934	Sequence 934, App	827	199.5	5.1	2556	1	US-08-185-432-17	Sequence 17, Appl
755	205	5.2	393	3	US-10-144-678A-934	Sequence 12, Appl	828	199.5	5.1	2556	1	US-08-083-590A-20	Sequence 20, Appl
756	204.5	5.2	360	3	US-10-162-335-12	Sequence 12, Appl	829	199.5	5.1	2556	2	US-08-532-384-20	Sequence 20, Appl

830	199.5	5.1	2556	2	US-08-899-232-2	Sequence 2, Appl1	903	195.5	5.0	2471	1	US-08-083-590A-19	Sequence 19, Appl1
831	199.5	5.1	2556	2	US-09-121-457-2	Sequence 2, Appl1	904	195.5	5.0	2471	2	US-08-532-384-19	Sequence 19, Appl1
832	199.5	5.0	2556	2	US-09-949-016-8151	Sequence 8151, Ap	905	195.5	5.0	2471	2	US-08-899-232-1	Sequence 1, Appl1
833	199.5	5.0	260	2	US-09-008-271A-7	Sequence 7, Appl1	906	195.5	5.0	2471	2	US-09-121-457-1	Sequence 1, Appl1
834	199.5	5.0	260	2	US-09-968-415-7	Sequence 4, Appl1	907	195.5	4.9	258	3	US-09-936-271C-85	Sequence 85, Appl1
835	199.5	5.0	278	1	US-08-392-828C-4	Sequence 4, Appl1	908	194.5	4.9	246	1	US-08-978-404B-4	Sequence 44, Appl1
836	199.5	5.0	278	2	US-09-330-945-9	Sequence 9, Appl1	909	194.5	4.9	341	3	US-10-162-335-20	Sequence 20, Appl1
837	198.5	5.0	223	1	US-08-278-091-9	Sequence 9, Appl1	910	194.5	4.9	415	2	US-09-032-523-2	Sequence 2, Appl1
838	198.5	5.0	223	1	US-08-483-859-9	Sequence 9, Appl1	911	194.5	4.9	415	2	US-09-802-633-2	Sequence 2, Appl1
839	198.5	5.0	223	1	US-08-472-173-9	Sequence 9, Appl1	912	194	4.9	113	3	US-09-438-046-20	Sequence 26, Appl1
840	198.5	5.0	223	1	US-08-487-167-9	Sequence 9, Appl1	913	194	4.9	113	3	US-09-410-362F-26	Sequence 26, Appl1
841	198.5	5.0	223	1	US-08-482-816-9	Sequence 9, Appl1	914	194	4.9	233	2	US-09-821-255-4	Sequence 4, Appl1
842	198.5	5.0	223	1	US-08-296-149-9	Sequence 9, Appl1	915	193.5	4.9	225	2	US-10-036-371-8	Sequence 8, Appl1
843	198.5	5.0	223	1	US-08-801-499-9	Sequence 9, Appl1	916	193	4.9	228	2	US-08-944-483-44	Sequence 44, Appl1
844	198.5	5.0	223	2	US-08-615-271-9	Sequence 9, Appl1	917	193	4.9	228	2	US-10-202-676-6	Sequence 69, Appl1
845	198.5	5.0	223	2	US-09-074-660-9	Sequence 9, Appl1	918	193	4.9	253	3	US-09-936-271C-69	Sequence 69, Appl1
846	198.5	5.0	223	2	US-09-074-659-9	Sequence 9, Appl1	919	193	4.9	253	7	5223425-8	Patent No. 5223425
847	198.5	5.0	223	2	US-09-106-468-9	Sequence 9, Appl1	920	193	4.9	268	2	US-09-032-215-42	Sequence 42, Appl1
848	198.5	5.0	223	2	US-09-106-467-9	Sequence 9, Appl1	921	192.5	4.9	225	1	US-08-557-146-12	Sequence 12, Appl1
849	198.5	5.0	223	2	US-09-601-318-2	Sequence 2, Appl1	922	192.5	4.9	225	1	US-08-557-146-12	Sequence 12, Appl1
850	198.5	5.0	223	2	US-09-120-582-2	Sequence 2, Appl1	923	192.5	4.9	226	2	US-09-154-344-12	Sequence 4, Appl1
851	198.5	5.0	229	2	US-09-949-016-10271	Sequence 2, Appl1	924	192.5	4.9	281	1	US-08-467-155A-7	Sequence 7, Appl1
852	198.5	5.0	849	2	US-08-978-404B-45	Sequence 45, Appl1	925	192.5	4.9	281	1	US-08-628-198-7	Sequence 7, Appl1
853	198.5	5.0	849	2	US-09-949-016-10271	Sequence 10271, A	926	192.5	4.9	281	2	US-09-201-038-7	Sequence 7, Appl1
854	198.5	5.0	221	2	US-08-944-483-57	Sequence 57, Appl1	927	192.5	4.9	281	3	US-10-021-368-7	Sequence 7, Appl1
855	197.5	5.0	221	2	US-08-944-483-54	Sequence 54, Appl1	928	192.5	4.9	281	5	PCT-US86-07343-7	Sequence 7, Appl1
856	197.5	5.0	222	1	US-08-456-840-46	Sequence 46, Appl1	929	192	4.9	149	2	US-09-518-046-20	Sequence 20, Appl1
857	197.5	5.0	222	1	US-08-466-407A-46	Sequence 46, Appl1	930	192	4.9	149	2	US-09-518-046-20	Sequence 20, Appl1
858	197.5	5.0	222	1	US-08-892-534A-46	Sequence 46, Appl1	931	191.5	4.9	221	2	US-09-650-371-20	Sequence 33, Appl1
859	197.5	5.0	248	2	US-10-012-231A-154	Sequence 194, App	932	191.5	4.9	221	2	US-09-959-393-33	Sequence 13, Appl1
860	197.5	5.0	248	2	US-10-012-231A-154	Sequence 194, App	933	191.5	4.9	224	2	US-08-766-982-13	Sequence 36, Appl1
861	197.5	5.0	248	2	US-10-006-768A-194	Sequence 194, App	934	191.5	4.9	224	2	US-08-944-483-36	Sequence 36, Appl1
862	197.5	5.0	248	2	US-10-015-671A-194	Sequence 194, App	935	191.5	4.9	225	1	US-09-027-337-5	Sequence 13, Appl1
863	197.5	5.0	248	2	US-10-011-833A-194	Sequence 194, App	936	191.5	4.9	225	2	US-09-644-600A-5	Sequence 5, Appl1
864	197.5	5.0	248	2	US-10-011-833A-194	Sequence 194, App	937	191.5	4.9	225	2	US-09-654-600A-5	Sequence 5, Appl1
865	197.5	5.0	248	2	US-10-006-041A-194	Sequence 194, App	938	191.5	4.9	225	3	US-09-421-213-5	Sequence 5, Appl1
866	197.5	5.0	248	2	US-10-012-064A-194	Sequence 194, App	939	191.5	4.9	233	2	US-09-636-382A-24	Sequence 24, Appl1
867	197.5	5.0	248	2	US-10-015-192A-194	Sequence 194, App	940	191.5	4.9	247	3	US-09-936-271C-82	Sequence 82, Appl1
868	197.5	5.0	248	3	US-10-011-795B-194	Sequence 194, App	941	191.5	4.9	579	2	US-10-094-744-1884	Sequence 1884, Ap
869	197.5	5.0	248	3	US-09-936-271C-60	Sequence 60, Appl1	942	191.5	4.9	830	1	US-08-110-158-4	Sequence 4, Appl1
870	197.5	5.0	248	3	US-10-012-121A-194	Sequence 194, App	943	191	4.8	250	7	5223425-4	Patent No. 5223425
871	197.5	5.0	248	3	US-10-015-186A-194	Sequence 194, App	944	191	4.8	254	2	US-09-439-311-525	Sequence 525, App
872	197.5	5.0	248	3	US-10-006-485A-194	Sequence 194, App	945	191	4.8	254	2	US-09-636-215-525	Sequence 525, App
873	197.5	5.0	248	3	US-10-006-746A-194	Sequence 194, App	946	191	4.8	254	2	US-09-685-166A-525	Sequence 525, App
874	197.5	5.0	248	3	US-10-012-752A-194	Sequence 194, App	947	191	4.8	254	2	US-09-679-426-525	Sequence 525, App
875	197.5	5.0	248	3	US-10-017-253A-194	Sequence 194, App	948	191	4.8	254	2	US-09-759-143-525	Sequence 525, App
876	197.5	5.0	248	3	US-10-015-519A-194	Sequence 194, App	949	191	4.8	254	2	US-09-651-236-525	Sequence 525, App
877	197.5	5.0	248	3	US-10-015-715A-194	Sequence 194, App	950	191	4.8	254	2	US-09-657-278-525	Sequence 525, App
878	197.5	5.0	248	3	US-10-007-236A-194	Sequence 194, App	951	191	4.8	254	2	US-10-012-896-525	Sequence 525, App
879	197.5	5.0	338	2	US-08-991-761A-10	Sequence 10, Appl1	952	191	4.8	254	3	US-09-936-271C-81	Sequence 81, Appl1
880	196.5	5.0	241	2	US-08-944-483-60	Sequence 60, Appl1	953	191	4.8	254	3	US-10-144-678A-525	Sequence 525, App
881	196.5	5.0	248	2	US-08-944-483-71	Sequence 71, Appl1	954	191	4.8	455	2	US-09-261-416-2	Sequence 2, Appl1
882	196.5	5.0	300	1	US-08-148-910-1	Sequence 1, Appl1	955	190.5	4.8	251	3	US-09-936-271C-77	Sequence 77, Appl1
883	196.5	5.0	300	1	US-08-448-937A-1	Sequence 1, Appl1	956	190	4.8	253	2	US-10-202-676-4	Sequence 4, Appl1
884	196.5	5.0	360	3	US-10-162-335-16	Sequence 16, Appl1	957	190	4.8	254	3	US-09-936-271C-81	Sequence 81, Appl1
885	196.5	5.0	2523	2	US-08-185-432-18	Sequence 18, Appl1	958	189.5	4.8	284	2	US-09-386-642-54	Sequence 54, Appl1
886	196.5	5.0	2523	2	US-08-899-232-3	Sequence 3, Appl1	959	189.5	4.8	284	2	US-10-026-606-1	Sequence 1, Appl1
887	196.5	5.0	2523	2	US-09-121-457-3	Sequence 45, Appl1	960	189.5	4.8	341	3	US-10-114-270-132	Sequence 132, App
888	196.5	5.0	232	2	US-08-944-483-45	Sequence 4, Appl1	961	189	4.8	220	2	US-09-352-616A-327	Sequence 327, App
889	195.5	5.0	241	1	US-08-330-978-4	Sequence 4, Appl1	962	189	4.8	220	2	US-09-232-148A-327	Sequence 327, App
890	195.5	5.0	241	1	US-08-474-042-4	Sequence 4, Appl1	963	189	4.8	220	2	US-09-636-215-327	Sequence 327, App
891	195.5	5.0	241	1	US-08-484-558-4	Sequence 4, Appl1	964	189	4.8	220	2	US-09-636-215-327	Sequence 327, App
892	195.5	5.0	241	1	US-08-774-592-3	Sequence 3, Appl1	965	189	4.8	220	2	US-09-688-166A-327	Sequence 327, App
893	195.5	5.0	241	1	US-08-330-978-4	Sequence 3, Appl1	966	189	4.8	220	2	US-09-688-489-327	Sequence 327, App
894	195.5	5.0	254	1	US-08-474-042-3	Sequence 3, Appl1	967	189	4.8	220	2	US-09-679-426-327	Sequence 327, App
895	195.5	5.0	254	1	US-08-484-558-3	Sequence 3, Appl1	968	189	4.8	220	2	US-09-759-143-327	Sequence 327, App
896	195.5	5.0	306	1	US-08-774-592-3	Sequence 3, Appl1	969	189	4.8	220	2	US-09-651-236-327	Sequence 327, App
897	195.5	5.0	306	1	US-08-330-978-1	Sequence 1, Appl1	970	189	4.8	220	2	US-09-657-279-327	Sequence 327, App
898	195.5	5.0	306	1	US-08-474-042-1	Sequence 1, Appl1	971	189	4.8	220	2	US-10-012-896-327	Sequence 327, App
899	195.5	5.0	306	1	US-08-484-558-1	Sequence 1, Appl1	972	189	4.8	220	2	US-10-144-678A-327	Sequence 327, App
900	195.5	5.0	309	2	US-08-774-592-1	Sequence 233, App	973	189	4.8	225	1	US-08-944-483-33	Sequence 33, Appl1
901	195.5	5.0	2471	1	US-10-360-101-233	Sequence 16, Appl1	974	189	4.8	225	1	US-09-027-337-4	Sequence 4, Appl1
902	195.5	5.0	2471	1	US-08-185-432-16	Sequence 16, Appl1	975	189	4.8	225	2	US-09-644-600-4	Sequence 4, Appl1

976	189	4.8	225	2	US-09-654-600A-4	Sequence 4, Appl1	1049	185.5	4.7	256	2	US-09-032-215-27	Sequence 27, Appl1
977	189	4.8	225	3	US-09-421-213-4	Sequence 2, Appl1	1050	185.5	4.7	261	2	US-08-163-919A-2	Sequence 2, Appl1
978	189	4.8	237	3	US-09-936-271C-2	Sequence 2, Appl1	1051	185.5	4.7	261	2	US-08-462-515-2	Sequence 2, Appl1
979	189	4.8	238	7	5223425-5	Patient No. 5223425	1052	185.5	4.7	261	5	PCT-US94-14073-2	Sequence 2, Appl1
980	189	4.8	253	1	US-08-557-146-2	Sequence 2, Appl1	1053	185.5	4.7	306	2	US-09-186-642-53	Sequence 53, Appl1
981	189	4.8	253	1	US-08-824-674-3	Sequence 3, Appl1	1054	185.5	4.7	711	1	US-08-184-012C-8	Sequence 8, Appl1
982	189	4.8	253	1	US-09-154-344-2	Sequence 2, Appl1	1055	185.5	4.7	711	1	US-08-334-177-2	Sequence 2, Appl1
983	189	4.8	253	2	US-08-930-188-2	Sequence 2, Appl1	1056	185.5	4.7	711	1	US-08-666-082B-1	Sequence 1, Appl1
984	189	4.8	253	2	US-09-210-084-3	Sequence 3, Appl1	1057	185.5	4.7	713	5	PCT-US95-13830-2	Sequence 2, Appl1
985	189	4.8	253	2	US-09-764-762-3	Sequence 3, Appl1	1058	185.5	4.7	713	2	US-08-872-855-5	Sequence 5, Appl1
986	189	4.8	253	3	US-10-071-214-2	Sequence 2, Appl1	1059	185	4.7	227	2	US-08-944-483-49	Sequence 49, Appl1
987	189	4.8	253	3	US-10-071-214-8	Sequence 48, Appl1	1060	185	4.7	258	1	US-08-744-026-3	Sequence 3, Appl1
988	189	4.8	253	5	PCT-US96-04294-2	Sequence 2, Appl1	1061	185	4.7	258	1	US-09-102-32-3	Sequence 3, Appl1
989	189	4.8	265	2	US-09-949-916A-7	Sequence 716, Ap	1062	185	4.7	258	2	US-09-261-767-3	Sequence 3, Appl1
990	189	4.8	312	2	US-09-023-942A-4	Sequence 4, Appl1	1063	185	4.7	314	2	US-09-023-942A-6	Sequence 6, Appl1
991	189	4.8	449	2	US-09-636-215-617	Sequence 617, App	1064	184	4.7	144	2	US-09-618-259-1	Sequence 1, Appl1
992	189	4.8	449	2	US-09-685-166A-617	Sequence 617, App	1065	184	4.7	144	3	US-08-915-659A-1	Sequence 1, Appl1
993	189	4.8	449	2	US-09-679-426-617	Sequence 617, App	1066	184	4.7	314	2	US-09-008-871A-3	Sequence 3, Appl1
994	189	4.8	449	2	US-09-759-143-617	Sequence 617, App	1067	184	4.7	314	2	US-09-907-794A-257	Sequence 257, App
995	189	4.8	449	2	US-09-651-236-617	Sequence 617, App	1068	184	4.7	314	2	US-09-905-125A-257	Sequence 257, App
996	189	4.8	449	2	US-09-657-279-617	Sequence 617, App	1069	184	4.7	314	2	US-09-902-775A-257	Sequence 257, App
997	189	4.8	449	2	US-10-012-896-617	Sequence 617, App	1070	184	4.7	314	2	US-09-906-700-257	Sequence 257, App
998	189	4.8	449	3	US-10-144-678A-617	Sequence 617, App	1071	184	4.7	314	2	US-09-903-603A-257	Sequence 257, App
999	189	4.8	585	3	US-10-144-678A-1020	Sequence 1020, Ap	1072	184	4.7	314	2	US-09-904-920A-257	Sequence 257, App
1000	188.5	4.8	290	2	US-09-386-653A-7	Sequence 7, Appl1	1073	184	4.7	314	2	US-09-909-064-257	Sequence 257, App
1001	188.5	4.8	290	2	US-10-040-655-7	Sequence 7, Appl1	1074	184	4.7	314	2	US-09-905-581A-257	Sequence 257, App
1002	188.5	4.8	290	2	US-10-041-054-7	Sequence 7, Appl1	1075	184	4.7	314	2	US-09-906-618-257	Sequence 257, App
1003	188	4.8	228	2	US-09-821-255-2	Sequence 2, Appl1	1076	184	4.7	314	2	US-09-906-646-257	Sequence 257, App
1004	188	4.8	248	1	US-08-744-026-1	Sequence 1, Appl1	1077	184	4.7	314	2	US-09-908-615-3	Sequence 3, Appl1
1005	188	4.8	248	1	US-09-102-732-1	Sequence 1, Appl1	1078	184	4.7	314	2	US-09-904-462-257	Sequence 257, App
1006	188	4.8	248	2	US-09-261-767-1	Sequence 1, Appl1	1079	184	4.7	314	2	US-09-902-736A-257	Sequence 257, App
1007	188	4.8	249	3	US-09-936-271C-68	Sequence 68, Appl1	1080	184	4.7	314	2	US-09-906-722A-257	Sequence 257, App
1008	188	4.8	254	2	US-10-202-676-2	Sequence 2, Appl1	1081	184	4.7	314	2	US-09-905-449-257	Sequence 257, App
1009	188	4.8	254	2	US-09-439-313-523	Sequence 523, App	1082	184	4.7	314	2	US-09-903-662B-257	Sequence 257, App
1010	188	4.8	254	2	US-09-636-215-523	Sequence 523, App	1083	184	4.7	314	2	US-09-906-679A-257	Sequence 257, App
1011	188	4.8	254	2	US-09-685-166A-523	Sequence 523, App	1084	184	4.7	314	3	US-09-907-841-257	Sequence 257, App
1012	188	4.8	254	2	US-09-679-426-523	Sequence 523, App	1085	183.5	4.7	502	2	US-10-099-322-140	Sequence 140, App
1013	188	4.8	254	2	US-09-759-143-523	Sequence 523, App	1086	183.5	4.7	502	2	US-10-044-564-140	Sequence 2, Appl1
1014	188	4.8	254	2	US-09-651-236-523	Sequence 523, App	1087	183.5	4.7	711	2	US-08-766-882-2	Sequence 2, Appl1
1015	188	4.8	254	2	US-09-657-279-523	Sequence 523, App	1088	183.5	4.7	711	2	US-09-296-219-2	Sequence 2, Appl1
1016	188	4.8	254	3	US-10-012-896-523	Sequence 523, App	1089	183.5	4.7	711	2	US-09-600-991-20	Sequence 20, Appl1
1017	188	4.8	254	3	US-10-144-678A-523	Sequence 523, App	1090	183.5	4.7	711	2	US-09-601-940A-12	Sequence 12, Appl1
1018	188	4.8	263	1	US-08-790-137-4	Sequence 4, Appl1	1091	183.5	4.7	711	2	US-09-949-016-6981	Sequence 6981, Ap
1019	188	4.8	263	1	US-08-824-874-5	Sequence 5, Appl1	1092	183.5	4.7	722	2	US-08-981-922-12	Sequence 12, Appl1
1020	188	4.8	263	2	US-08-807-151-5	Sequence 5, Appl1	1093	183.5	4.7	722	2	US-09-908-122-12	Sequence 12, Appl1
1021	188	4.8	263	2	US-09-210-084-5	Sequence 5, Appl1	1094	183	4.6	418	2	US-10-177-661-6	Sequence 6, Appl1
1022	188	4.8	263	2	US-09-478-957-5	Sequence 5, Appl1	1095	182.5	4.6	258	2	US-09-023-942A-8	Sequence 8, Appl1
1023	188	4.8	263	2	US-09-764-762-5	Sequence 8, Appl1	1096	182.5	4.6	484	1	US-08-252-193C-9	Sequence 9, Appl1
1024	188	4.8	263	2	US-08-991-761A-8	Sequence 8, Appl1	1097	182.5	4.6	484	2	US-09-276-197-9	Sequence 9, Appl1
1025	187.5	4.8	224	2	US-08-944-483-35	Sequence 35, Appl1	1098	182.5	4.6	720	2	US-08-872-855-4	Sequence 4, Appl1
1026	187.5	4.8	224	2	US-08-944-483-29	Sequence 29, Appl1	1099	182.5	4.6	722	2	US-09-310-885-14	Sequence 14, Appl1
1027	187.5	4.8	255	2	US-08-906-769-83	Sequence 83, Appl1	1100	182	4.6	405	2	US-09-734-675-2	Sequence 2, Appl1
1028	187.5	4.8	255	2	US-08-906-616-83	Sequence 83, Appl1	1101	182	4.6	405	2	US-10-060-333-2	Sequence 2, Appl1
1029	187.5	4.8	255	2	US-08-817-795-83	Sequence 83, Appl1	1102	182	4.6	721	2	US-08-872-855-7	Sequence 7, Appl1
1030	187.5	4.8	255	2	US-08-639-075A-83	Sequence 83, Appl1	1103	182	4.6	1055	2	US-09-214-778-2	Sequence 2, Appl1
1031	187.5	4.8	255	2	US-09-012-431-83	Sequence 83, Appl1	1104	182	4.6	1055	2	US-09-855-122-2	Sequence 2, Appl1
1032	187.5	4.8	255	2	US-09-012-692-83	Sequence 83, Appl1	1105	182	4.6	1065	1	US-08-400-159-8	Sequence 8, Appl1
1033	187.5	4.8	255	2	US-08-906-613-83	Sequence 83, Appl1	1106	182	4.6	1212	2	US-09-214-778-3	Sequence 3, Appl1
1034	187.5	4.8	255	5	PCT-US95-14442A-83	Sequence 83, Appl1	1107	182	4.6	1212	2	US-09-855-122-3	Sequence 3, Appl1
1035	187	4.7	296	3	US-09-936-271C-22	Sequence 22, Appl1	1108	182	4.6	1238	2	US-09-214-778-5	Sequence 5, Appl1
1036	187	4.7	693	3	US-10-297-895A-12	Sequence 20, Appl1	1109	182	4.6	1238	2	US-09-855-122-5	Sequence 5, Appl1
1037	187	4.7	1004	2	US-10-114-270-32	Sequence 32, Appl1	1110	182	4.6	1257	2	US-08-611-129A-8	Sequence 8, Appl1
1038	186	4.7	110	2	US-09-341-461-38	Sequence 28, Appl1	1111	182	4.6	1257	2	US-09-195-524-8	Sequence 8, Appl1
1039	186	4.7	230	1	US-08-456-840-47	Sequence 47, Appl1	1112	182	4.6	1257	2	US-09-310-685-6	Sequence 6, Appl1
1040	186	4.7	230	1	US-08-266-407A-47	Sequence 47, Appl1	1113	181.5	4.6	256	1	US-07-990-501A-2	Sequence 2, Appl1
1041	186	4.7	230	1	US-08-892-544-47	Sequence 47, Appl1	1114	181.5	4.6	299	1	US-08-467-155A-8	Sequence 8, Appl1
1042	186	4.7	230	1	US-08-766-982-12	Sequence 12, Appl1	1115	181.5	4.6	299	1	US-08-628-198-8	Sequence 8, Appl1
1043	186	4.7	230	2	US-08-944-483-53	Sequence 53, Appl1	1116	181.5	4.6	299	2	US-09-201-038-8	Sequence 8, Appl1
1044	186	4.7	230	2	US-09-296-219-12	Sequence 12, Appl1	1117	181.5	4.6	299	3	US-10-021-368-8	Sequence 8, Appl1
1045	186	4.7	232	1	US-08-897-340-31	Sequence 31, Appl1	1118	181.5	4.6	299	5	PCT-US96-07343-8	Sequence 8, Appl1
1046	186	4.7	232	2	US-09-252-329-31	Sequence 31, Appl1	1119	181	4.6	257	3	US-09-936-271C-87	Sequence 87, Appl1
1047	186	4.7	326	2	US-09-411-977-3	Sequence 3, Appl1	1120	181	4.6	396	2	US-09-800-729-86	Sequence 86, Appl1
1048	186	4.7	326	2	US-10-057-951-3	Sequence 3, Appl1	1121	180	4.6	249	3	US-10-071-214-47	Sequence 47, Appl1

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1123	180	4.6	254	3	US-09-936-271C-59	Sequence 59, App1	1196	176.5	4.5	914	2	US-08-936-135-12	Sequence 12, App1
1124	180	4.6	260	7	5223425-10	Patent No. 5223425	1197	176.5	4.5	914	2	US-09-439-711C-12	Sequence 12, App1
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1126	179.5	4.6	205	2	US-09-030-607-176	Sequence 176, App	1199	176.5	4.5	925	2	US-08-936-135-15	Sequence 14, App1
1127	179.5	4.6	205	2	US-09-439-913-176	Sequence 176, App	1200	176.5	4.5	926	2	US-09-439-711C-14	Sequence 14, App1
1128	179.5	4.6	205	2	US-09-352-616A-176	Sequence 176, App	1201	176.5	4.5	931	2	US-08-936-135-16	Sequence 16, App1
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1133	179.5	4.6	205	2	US-09-115-453-176	Sequence 176, App	1206	176	4.5	232	2	US-08-944-483-58	Sequence 58, App1
1134	179.5	4.6	205	2	US-09-688-489-176	Sequence 176, App	1207	176	4.5	266	2	US-09-004-731-24	Sequence 24, App1
1135	179.5	4.6	205	2	US-09-679-426-176	Sequence 176, App	1208	176	4.5	266	2	US-08-749-699-24	Sequence 24, App1
1136	179.5	4.6	205	2	US-09-759-143-176	Sequence 176, App	1209	176	4.5	266	2	US-09-004-729-24	Sequence 24, App1
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1138	179.5	4.6	205	2	US-09-030-606-176	Sequence 176, App	1211	175.5	4.4	266	2	US-09-004-729-24	Sequence 24, App1
1139	179.5	4.6	205	2	US-09-657-279-176	Sequence 176, App	1212	175	4.4	921	2	US-09-439-711C-46	Sequence 46, App1
1140	179.5	4.6	205	2	US-10-012-896-176	Sequence 176, App	1213	175	4.4	112	2	US-09-439-711C-21	Sequence 21, App1
1141	179.5	4.6	205	3	US-09-116-134-176	Sequence 176, App	1214	175	4.4	909	2	US-08-936-135-18	Sequence 18, App1
1142	179.5	4.6	250	3	US-10-144-678A-176	Sequence 176, App	1215	175	4.4	909	2	US-09-439-711C-18	Sequence 18, App1
1143	179.5	4.6	250	3	US-09-936-271C-23	Sequence 23, App	1216	175	4.4	926	2	US-09-439-711C-20	Sequence 20, App1
1144	179.5	4.6	259	7	5223425-2	Patent No. 5223425	1217	175	4.4	931	2	US-09-583-638-4	Sequence 4, App1
1145	179.5	4.6	728	2	US-08-981-392-2	Sequence 2, App1	1218	174	4.4	265	1	US-08-177-109A-57	Sequence 57, App1
1146	179.5	4.6	728	2	US-09-908-322-2	Sequence 2, App1	1219	174	4.4	265	1	US-08-687-706-57	Sequence 57, App1
1147	179.5	4.6	728	2	US-09-310-685-11	Sequence 11, App1	1220	174	4.4	266	1	US-08-467-155A-9	Sequence 9, App1
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1149	179	4.5	220	1	US-08-379-621-2	Sequence 2, App1	1222	174	4.4	286	2	US-09-201-038-9	Sequence 9, App1
1150	179	4.5	220	1	US-08-147-000B-2	Sequence 2, App1	1223	174	4.4	286	2	US-10-021-368-9	Sequence 9, App1
1151	179	4.5	230	1	US-08-889-078-2	Sequence 2, App1	1224	174	4.4	286	3	PCT-US96-07343-9	Sequence 9, App1
1152	179	4.5	253	2	US-09-578-303-4	Sequence 4, App1	1225	173.5	4.4	286	3	US-10-360-101-222	Sequence 22, App
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1154	178.5	4.5	350	2	US-08-944-483-68	Sequence 68, App1	1227	173.5	4.4	294	2	US-10-067-422-12	Sequence 12, App1
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1157	178.5	4.5	401	1	US-10-041-054-9	Sequence 9, App1	1230	173	4.4	211	2	US-09-320-731-25	Sequence 25, App1
1158	178.5	4.5	468	1	US-08-839-008-5	Sequence 5, App1	1231	173	4.4	449	1	US-09-242-999-20	Sequence 20, App1
1159	178.5	4.5	468	2	US-08-839-008-7	Sequence 7, App1	1232	172.5	4.4	449	1	US-08-839-008-2	Sequence 2, App1
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1164	178.5	4.5	923	2	US-09-439-711C-6	Sequence 6, App1	1237	172.5	4.4	571	2	US-10-145-129A-132	Sequence 132, App
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1178	177	4.5	240	1	US-08-801-499-11	Sequence 11, App1	1251	171.5	4.3	259	2	US-08-906-769-190	Sequence 190, App
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1186	177	4.5	830	7	5378464-2	Patent No. 5378464	1259	171.5	4.3	259	2	US-09-004-729-85	Sequence 85, App1
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1189	176.5	4.5	901	2	US-09-439-711C-22	Sequence 22, App1	1262	171.5	4.3	262	1	US-08-824-874-4	Sequence 4, App1
1190	176.5	4.5	906	2	US-08-936-135-24	Sequence 24, App1	1263	171.5	4.3	262	1	US-08-824-874-4	Sequence 4, App1
1191	176.5	4.5	906	2	US-09-439-711C-24	Sequence 24, App1	1264	171.5	4.3	262	2	US-08-807-151-4	Sequence 4, App1
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1194	176.5	4.5	909	2	US-09-439-711C-8	Sequence 8, App1	1267	171.5	4.3	262	2	US-09-764-762-4	Sequence 4, App1

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ALIGNMENTS

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: RESULT 1 - 181-231
: US-09-991-181-231
: Sequence 231, Application US/09991181
: Patent No. 691319
: GENERAL INFORMATION:
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: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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: PRIOR FILING DATE: 1998-05-28

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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 2; Length 720;
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Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-990-444-231
Sequence 231, Application US/09990444
Patent No. 6930170
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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;; PRIOR APPLICATION NUMBER: 60/091978
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 VVGTTIPCCNNEBNECDSCIHPGCTIFENCKSCRNGSGTLDYFYVKGFYCAEGRAG 120
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Qy 181 YVEVRDGNDRDQGIIRKVCNENRPAPIQISGSSLHLVLFHSDGSKNDFGHAITYEETIAGS 240
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RESULT 3
US-09-997-333-231
Sequence 231, Application US/09997333
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC27
CURRENT APPLICATION NUMBER: US/09/997,333
PRIOR APPLICATION NUMBER: 2001-11-15
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1997-10-17
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 RESULT 4
 US-09-992-598-231
 Sequence 231, Application US/09992598
 Patent No. 6956108
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Ferrara, Daniele
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gettitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Nepier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: F2730PIC20
CURRENT FILING DATE: 2001-11-14
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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QY      121 YGSDCMRGQVLRAPKQIILLESYPLNACWMTTHAKGFYIQLRFVWLSLEFDYMCQYD 180
DB      121 YGSDCMRGQVLRAPKQIILLESYPLNACWMTTHAKGFYIQLRFVWLSLEFDYMCQYD 180
QY      121 YGSDCMRGQVLRAPKQIILLESYPLNACWMTTHAKGFYIQLRFVWLSLEFDYMCQYD 180
DB      121 YGSDCMRGQVLRAPKQIILLESYPLNACWMTTHAKGFYIQLRFVWLSLEFDYMCQYD 180
QY      181 YVEVRDGNRGGQIIKRVCGNERPAPISIGSSILHVLPHSGSKNPFQSFHAIYEETIACS 240
DB      181 YVEVRDGNRGGQIIKRVCGNERPAPISIGSSILHVLPHSGSKNPFQSFHAIYEETIACS 240
QY      241 SSPCFHDTCVLDKXGSKYKACLAGYTQRCENILLEBNRNCSDPGPVNGYOKITGGPGLI 300
DB      241 SSPCFHDTCVLDKXGSKYKACLAGYTQRCENILLEBNRNCSDPGPVNGYOKITGGPGLI 300
QY      301 NGRHAKTGVVSFFCNSNYSVLGNEKRTCCQNGEWSGKOPICIKACREPKISDLVRRVVL 360
DB      301 NGRHAKTGVVSFFCNSNYSVLGNEKRTCCQNGEWSGKOPICIKACREPKISDLVRRVVL 360
QY      361 PMOVOSRRTPLHQLYSAAFSKOKLOSAPTKKPALPBGDLPMGYQHLHQLQLOECISPPYR 420
DB      361 PMOVOSRRTPLHQLYSAAFSKOKLOSAPTKKPALPBGDLPMGYQHLHQLQLOECISPPYR 420

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QY      481 HKGAWFLVCSGALVNERVTYVVAHCTTDDIGKTYMTADLKVYLGFYRDDDDREDEKTIOS 540
DB      481 HKGAWFLVCSGALVNERVTYVVAHCTTDDIGKTYMTADLKVYLGFYRDDDDREDEKTIOS 540
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DB      541 LQISATIIHPNYPIILLDDIALILKLLDKARISTRVQPICLAASRDLSTSFQESHITTVAG 600
QY      601 MWNLADVRSPGFNDTLRSGVSVVDSLLCEEQHEHDGIPVSVTDNMFCASMEPTAPSDI 660
DB      601 MWNLADVRSPGFNDTLRSGVSVVDSLLCEEQHEHDGIPVSVTDNMFCASMEPTAPSDI 660
QY      661 CTAEITGIIAIVSPFGASPEPRRWHLMGVYSKSDTKCSHRLSTAFKVLPRFKWIRRNK 720
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RESULT 5

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US-09-989-735-231
; Sequence 231, Application US/09989735
; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavrin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1c61
; CURRENT APPLICATION NUMBER: US/09/989, 735
; CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 2; Length 720;
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DB 61 VGGTIFCCRNNEECSCLIHPGCTTFENCKSCRNSMGCTLDDFYVKGFYCAECAGW 120
QY 121 YGGDCMRGCVLRAPKQIILLESYPLNAHCMTIHAKEGFIQLRFYMLSLFPDYMCOYD 180
DB 121 YGGDCMRGCVLRAPKQIILLESYPLNAHCMTIHAKEGFIQLRFYMLSLFPDYMCOYD 180
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DB 181 YVEVRDDNDRDQIIRKVCGERPAPIQSIGSLHVLPHSDGKDFGFAIYEITACS 240
QY 241 SSPCFHDTGCVLDKAGSYKACLAGYTGRCENTLEBRNCSDPGAPVNGYOKITGGGGLI 300
DB 241 SSPCFHDTGCVLDKAGSYKACLAGYTGRCENTLEBRNCSDPGAPVNGYOKITGGGGLI 300
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GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Deenoyers, Luc
;; APPLICANT: Eacon, Dan L.
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
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QY 121 YGSDCKRCQVLRAPRGQILLESYPINAHCEWTIAKPGFVQLRPFVMSLEFDYMCQYD 180
DB 121 YGSDCKRCQVLRAPRGQILLESYPINAHCEWTIAKPGFVQLRPFVMSLEFDYMCQYD 180
QY 121 YGSDCKRCQVLRAPRGQILLESYPINAHCEWTIAKPGFVQLRPFVMSLEFDYMCQYD 180
DB 121 YGSDCKRCQVLRAPRGQILLESYPINAHCEWTIAKPGFVQLRPFVMSLEFDYMCQYD 180
QY 181 YVEVRGDNRRDQIIRKVGNERPAPISIGSLHVLFFSDSKNDGSHAIYEETIACS 240
DB 181 YVEVRGDNRRDQIIRKVGNERPAPISIGSLHVLFFSDSKNDGSHAIYEETIACS 240
QY 241 SSPCFHDGTCVLDKAGSYKACIAGYTGRCENLLEERNCSDPGPGVNGYOKITGPGGLI 300
DB 241 SSPCFHDGTCVLDKAGSYKACIAGYTGRCENLLEERNCSDPGPGVNGYOKITGPGGLI 300
QY 301 NGRHAKITGVVSFFCNNSYVLSGNERKTQONGEWSGKOPICIKACREBKISDLVRRVYL 360
DB 301 NGRHAKITGVVSFFCNNSYVLSGNERKTQONGEWSGKOPICIKACREBKISDLVRRVYL 360
QY 361 PMOVOSRETPHLQLYSAAFSKQLQSAPTKKPALPGDLPWGQHLTLQYECISPFYR 420
DB 361 PMOVOSRETPHLQLYSAAFSKQLQSAPTKKPALPGDLPWGQHLTLQYECISPFYR 420

QY 421 RLSSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTOGLRMPQOAIYRTSGVHDGSL 480
DB 421 RLSSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTOGLRMPQOAIYRTSGVHDGSL 480
QY 481 HKGAMFLVCSGALVNEKTVVAHCVTDLCKVTMIKTADIKVYLKGYRDDDEKTIQS 540
DB 481 HKGAMFLVCSGALVNEKTVVAHCVTDLCKVTMIKTADIKVYLKGYRDDDEKTIQS 540
QY 541 LQISATILHNPYDILADADIALIKLIDKARISRVOPICLASRDLSFQESHITVAG 600
DB 541 LQISATILHNPYDILADADIALIKLIDKARISRVOPICLASRDLSFQESHITVAG 600
QY 601 MNVLADVRSPGKNDTLRSQVSVYDSSLCEQEHEDGIPVSYTDNMFCASWEPTAPSDI 660
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QY 661 CTMETGGAIVSPGRASPEPRMHLMGLVMSYDKTCSHRLSTAFTYKVLPPKQMIERNMK 720
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RESULT 7
US-09-997-514-231
Sequence 231, Application US/09997514
Patent No. 7019116
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
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APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C46
CURRENT APPLICATION NUMBER: US/09/997,514
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
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 ; PRIOR APPLICATION NUMBER: 60/091978

; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09
 Query Match 100.0%; Score 3945; DB 3; Length 720;
 Best Local Similarity 100.0%; Pred. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 720; Conservative 0;

QY 1 MELGCTWQGLTFLQLLISLPREXTVINEACPGAENWIMRECECEYDQIECVGPKBE 60
 DB 1 MELGCTWQGLTFLQLLISLPREXTVINEACPGAENWIMRECECEYDQIECVGPKBE 60
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 DB 61 VVGYYTTPCCRNENECDSCLIHGCTTFENCKSCRNCSNGVGLDDFYVKGFTCAECRAGM 120
 QY 121 YGGDCMRGCGVLRAPRGQILLESYPLNACEWTHAKPFFVQLRPMVLSLEFDVWCQYD 180
 DB 121 YGGDCMRGCGVLRAPRGQILLESYPLNACEWTHAKPFFVQLRPMVLSLEFDVWCQYD 180
 QY 181 YVEVRDGNRDQOIIKRVCGNERPAPIOSIGSSLHYLFSDSDSKNPDGFHAHYEEITFAS 240
 DB 181 YVEVRDGNRDQOIIKRVCGNERPAPIOSIGSSLHYLFSDSDSKNPDGFHAHYEEITFAS 240
 QY 241 SSPCFHDTGTCVLDKAGSYKACLAGYTGRCENTLEERNCSDPGPFVNGYQKITGGPGLI 300
 DB 241 SSPCFHDTGTCVLDKAGSYKACLAGYTGRCENTLEERNCSDPGPFVNGYQKITGGPGLI 300
 QY 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOONGMSGKOPICIKACREKISDLYVRRVL 360
 DB 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOONGMSGKOPICIKACREKISDLYVRRVL 360
 QY 361 PMOVOSRETPHLQVLSAASFKXKALPFGDPMGVOHLHTLOJECISPFYR 420
 DB 361 PMOVOSRETPHLQVLSAASFKXKALPFGDPMGVOHLHTLOJECISPFYR 420
 QY 421 RLGSSRRCTLRGKMSGRAPSCIPICGIENITAPRTQGLRPMWQAIYRRRTSGVHDSGL 480
 DB 421 RLGSSRRCTLRGKMSGRAPSCIPICGIENITAPRTQGLRPMWQAIYRRRTSGVHDSGL 480
 QY 481 HKGAMFLVCSGALVNERTVVAACHCTDYGKVTMTADLKVYLGFYDDDDREDEXTIOS 540
 DB 481 HKGAMFLVCSGALVNERTVVAACHCTDYGKVTMTADLKVYLGFYDDDDREDEXTIOS 540
 QY 541 LQISATILHPNDPILDDADIALKLDKARISTRVQPICLAASRDLSFSFQESHITTVAG 600
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 QY 601 MNVLADVRSPGFNDTLRSGVSVVDSLLCEQHEHDGIPVSVTDNMPFCASMEPTAPSDI 660
 DB 601 MNVLADVRSPGFNDTLRSGVSVVDSLLCEQHEHDGIPVSVTDNMPFCASMEPTAPSDI 660
 QY 661 CTAEITGIAVSPFGASPEPRHMLGLVSWSYDKTCSRHLSTAFTKVLPFKOWIRRNK 720
 DB 661 CTAEITGIAVSPFGASPEPRHMLGLVSWSYDKTCSRHLSTAFTKVLPFKOWIRRNK 720

RESULT 8
 US-09-989-728-231
 ; Sequence 231, Application US/09989728
 ; Patent No. 7029873
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Rong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavini, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PLC72
 CURRENT APPLICATION NUMBER: US/09/989,728
 PRIOR FILING DATE: 2001-11-20
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 YGGDCMRCGVVLAPKQIILLESPLNAHCEWTHARGVYQIRFVMSLEPYMCYD 180
QY 181 YVEVRDNDNGOIKKVCNERNAPQISIGSSLHV FHS DGSNGPFGFAIYEETAC 240
DB 181 YVEVRDNDNGOIKKVCNERNAPQISIGSSLHV FHS DGSNGPFGFAIYEETAC 240
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DB 241 SSPCFHDTCLVDKAGSYKACLAGYTGRCENLLEBRNCSDPGPNVGYOKITGPGLI 300
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RESULT 9
US-09-997-349-231
Sequence 231, Application US/09997349
Patent No. 7034106
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey E.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC37
CURRENT APPLICATION NUMBER: US/09/997,349
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28


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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 3945; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 231, Application US/09997653
; Patent No. 7034122
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
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; APPLICANT: Botsstein, David
; APPLICANT: Deenoyers, Luc
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; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C38
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PROR FILING DATE: 1998-07-07
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PROR FILING DATE: 1998-07-07
PROR APPLICATION NUMBER: 60/092182
PROR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 VVGTTTCCNENECNESCILHFGCTTFENCKSCRNCSWGGTDDDFYKGFYCAECRAGW 120

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Db 361 PMQVGRREFPLHQLYSAARSKQLQSAFTKKPALPFQDLPWGQHLHTQLOVEYCISPFPR 420
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Db 421 RLSSSRRTCLRTKMGSRAPSCPIPGKIENTIAPTQGLRWQOAIYRRTISGVHDGSI 480
QY 481 HKGAWFLVSGALVNRVTVAACHCTDGLKVMITADLKVGLGKPYDDEDEXTIOS 540
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RESULT 11
US-09-989-293A-231
Sequence 231, Application US/09989293A
Patent No. 7034136
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989, 293A
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633

;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MELGCTQLGLTFLQLLLSSLPREYTVINEACPGAEWNIWCECEYDIECCPGKRE 60
Db 1 MELGCTQLGLTFLQLLLSSLPREYTVINEACPGAEWNIWCECEYDIECCPGKRE 60
Qy 61 VVGTTTCCNNEECDSCLIHGCTTFENCKSCRNKSGWGTLDFFVKGFFCAECRAGW 120
Db 61 VVGTTTCCNNEECDSCLIHGCTTFENCKSCRNKSGWGTLDFFVKGFFCAECRAGW 120
Qy 121 YGGDCMKCGVLRAPKQIILLESYPLNAHCEWTHAKPGFVQLRFVMLSLEFDYMCQYD 180
Db 121 YGGDCMKCGVLRAPKQIILLESYPLNAHCEWTHAKPGFVQLRFVMLSLEFDYMCQYD 180
Qy 181 YVEVRDGNRDQIIRKVCNERNPAPQISIGSSLHVLFHSDSGNFDFHAIYEETAC 240
Db 181 YVEVRDGNRDQIIRKVCNERNPAPQISIGSSLHVLFHSDSGNFDFHAIYEETAC 240
Qy 241 SSPCFHDGTCLVLDKASGYKACIAGTGORCENULLEBRNCSDPGPGVNGYQKITGPGLI 300
Db 241 SSPCFHDGTCLVLDKASGYKACIAGTGORCENULLEBRNCSDPGPGVNGYQKITGPGLI 300
Qy 301 NGRHAKIGTVSFFCNNSVYLSGNEKRTCOQNGEMSGKOPCTIKAREPKISLVRRVYL 360
Db 301 NGRHAKIGTVSFFCNNSVYLSGNEKRTCOQNGEMSGKOPCTIKAREPKISLVRRVYL 360
Qy 361 PMQVQSRRTPLHQLYSAAFSKQLOSAPTKKPALPMGYOHLHTOLOVCISPFYR 420
Db 361 PMQVQSRRTPLHQLYSAAFSKQLOSAPTKKPALPMGYOHLHTOLOVCISPFYR 420
Qy 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPYTOGIRMPWQAAIYRTSGVHDSL 480
Db 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPYTOGIRMPWQAAIYRTSGVHDSL 480
Qy 481 HKGAMFLVCSGALVNEETVVAACHCTDLAGKMTITADLKVLYGFRDDDEXTIOS 540
Db 481 HKGAMFLVCSGALVNEETVVAACHCTDLAGKMTITADLKVLYGFRDDDEXTIOS 540
Qy 541 LQISATILHNPYDPIILDADIALIKLDRKARISTRVOPICLAASRDLSTFQESHITVAG 600
Db 541 LQISATILHNPYDPIILDADIALIKLDRKARISTRVOPICLAASRDLSTFQESHITVAG 600
Qy 601 WNVLDVRSFGPNVDLTRSGVSVVDLCEQEHEDHGIPVSYTDNNFCASWEPTAPSDI 660
Db 601 WNVLDVRSFGPNVDLTRSGVSVVDLCEQEHEDHGIPVSYTDNNFCASWEPTAPSDI 660
Qy 661 CTABTGIAVSPFGASPRPRWHLMLGVSWSDKTSRHLSTAFKTVLPFKWMIRNNK 720
Db 661 CTABTGIAVSPFGASPRPRWHLMLGVSWSDKTSRHLSTAFKTVLPFKWMIRNNK 720

RESULT 12

US-10-067-422-9
Sequence 9, Application US/10067422
Patent No. 6743613
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and
FILE REFERENCE: P7004P1
CURRENT APPLICATION NUMBER: US/10/067,422
CURRENT FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 09/685,899

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; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: PCT/US00/09028
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/152,933
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/147,020
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/131,672
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/130,693
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-422-9
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Query Match      74.7%; Score 2946.5; DB 2; Length 570;
Best Local Similarity 96.8%; Pred. No. 8.4e-237;
Matches 552; Conservative 0; Mismatches 1; Indels 17; Gaps 1;
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QY 168 MSLSEFDYMCQYDVEYVRDGDNRDGOIIRKVCGERPAPISIGSSLHLVLFHSDGSKNFD 227
DB 1 MSLSEFDYMCQYDVEYVRDGDNRDGOIIRKVCGERPAPISIGSSLHLVLFHSDGSKNFD 60
QY 228 GFHAIEITACSSSPCFHDTGTCVLDAKSGYKACAGYTGRCENTL----- 274
DB 61 GFHAIEITACSSSPCFHDTGTCVLDAKSGYKACAGYTGRCENTLLEAGSKIKASED 120
QY 275 -----LEERNCSDDGPNNGYQKITGPGGLNGRRAKIGTVVSFFCNNSYLSGNEKRTQ 330
DB 121 SLSSLEERNCSDDGPNNGYQKITGPGGLNGRRAKIGTVVSFFCNNSYLSGNEKRTQ 180
QY 331 QNEMSGKOPICIKACREPKISDLVRRRLVPMOVOSRETPHOLYSAFQKOLQSAPTK 390
DB 181 QNEMSGKOPICIKACREPKISDLVRRRLVPMOVOSRETPHOLYSAFQKOLQSAPTK 240
QY 391 KPALPGDLPNGYOHHTLOQYECISPFYRRLGSSRRRTCLRTGKMSGRABSCIPICGKIE 450
DB 241 KPALPGDLPNGYOHHTLOQYECISPFYRRLGSSRRRTCLRTGKMSGRABSCIPICGKIE 300
QY 451 NITAPRTQGLRWMOAIIYRTSGVHDSLHKGAMPLVCSGALVNERTVVAACHCTDLC 510
DB 301 NITAPRTQGLRWMOAIIYRTSGVHDSLHKGAMPLVCSGALVNERTVVAACHCTDLC 360
QY 511 KVTMIKTADLVKVLGKFRYDDDDREKTIQSLQISAILHBNYDPIILDADIALIKLIDKA 570
DB 361 KVTMIKTADLVKVLGKFRYDDDDREKTIQSLQISAILHBNYDPIILDADIALIKLIDKA 420
QY 571 RISTRVOPICLAASRDLSFQESHITVAGMNVLAADVSPGFKNIDTLRSQVSVSDSLC 630
DB 421 RISTRVOPICLAASRDLSFQESHITVAGMNVLAADVSPGFKNIDTLRSQVSVSDSLC 480
QY 631 EEEHEDHGIPVSTDMNFCASWEPTASDICTAETGIAAVSPFGRASPEPRHMLGLVS 690
DB 481 EEEHEDHGIPVSTDMNFCASWEPTASDICTAETGIAAVSPFGRASPEPRHMLGLVS 540
QY 691 WSYDKTCSHRLSTAFTKVLFPKDMIERNMK 720
DB 541 WSYDKTCSHRLSTAFTKVLFPKDMIERNMK 570
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RESULT 13
US-10-183-992-4
; Sequence 4, Application US/10183992
; Patent No. 6848426
; GENERAL INFORMATION:
; APPLICANT: Chen, Lin
; APPLICANT: Pepe, Michael
; TITLE OF INVENTION: Methods and Reagents for Detecting Endotoxin
; FILE REFERENCE: 02877.00008
```

```

; CURRENT APPLICATION NUMBER: US/10/183,992
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/310,125
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Tachypleudus tridentata
US-10-183-992-4
```

```

Query Match      17.0%; Score 672; DB 2; Length 1019;
Best Local Similarity 25.6%; Pred. No. 5e-47;
Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;
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QY 34 PGAEWNIM-----CRECEYDQIE---CYCPGKREVVGYTIPCCRNENECDCLIHPGCT 86
DB 184 PNGQSSFPKICRECAKASSPEHGKVNAPSGNMIEGATL-----RFSCDS-----PYUL 233
QY 87 IFENCKSCR-NGSWGTL----- 103
DB 234 ICGETLTCQNGQMSGQIPQCKKLVFCPDLDPVNAEHQVIGVEQKYGQFPGTEVYTT 293
QY 104 ---DDFYVKGFCACER--AGWYGG--DCMR-----CGQYLR--APKG 137
DB 294 CSGNYFLMGFNTLKCNPDSGMSGQSPSCVAVADREYDCSKAVDLDVGEPRIRHCPAG 353
QY 138 QILLES-----YPLNHCERTIHA---KPGFVI----- 163
DB 354 CSTLACTAGTCAIYHLLSSVCRAIHAGLCPNSGAVHYVNNPYSDFLGSDLNGIKSE 413
QY 164 LRFVMSLEFDYMCQYDVEYVRDGDNRDGOIIRKVCGERPAPISIGSSLHLVLFHSDGSKNFD 227
DB 414 LKSLARSPREDYVSSSTAGSGCPDMFEVEECVYVTSKORAMERBAQCVTMAARLAV 473
QY 207 IQS--IGSSLHLVLFHSDGSKNFDGPH-----AIYEITACSSSPCF 245
DB 474 LDKDLIPSSLTETLRGKGLTTWIGHRLDAEKFPWELMDRSNNVJNLNLTFWASGEPG 533
QY 246 HDGTCV-LDKAGS---YKACIAGYTGRCENTLEERN---CSDPGPNNGYQKITGPG 297
DB 534 NETNVCYLLDIRDOLQVWMTKSCFQPSFACMDLSDRKAKCDDPGPLENGHATLHGOS 593
QY 298 GLINGHAKIGTVVSFFCNNSYLSGNEKRTQONEMSGKOPICIK--ACREPKISDLV 355
DB 594 --IDGFYA--GSSIRSCVHLHLSGTEITVCTTGTGWSAPKRCIKVITCQNPVPYSYG 649
QY 356 RRRVLEPMOVOSRETPHOLYSAFQKOLQ---SAFTKAPALPGD-----LP 400
DB 650 SVRIKP---PSRNSISRVGSPFLRLPLPLPARAKPPKPRSSQSPSTVDLASKVKLP 706
QY 401 MGYOHHTLOQYECISPFYRRLGSSRRRTCLRTGKMSGRABSCIPICGKIENTIAP----- 455
DB 707 EGHYVGSRAIYICSERYIELLGSQGRCDSONMSGRPASCLPVCGRSQSPSPPTWNG 766
QY 456 -KTQGLRWMOAIIYRTSGVHDSLHKGAMPLVCSGALVNERTVVAACHCTDLCVTM 514
DB 767 NSTEIQGMWPMQAGISMLA-----DHMMWFLQGGGSLNEMKWIYTAHACVYTSATFI 819
QY 515 IKTADLVKVLGKFRYDDDDREKTIQSLQISAILHBNYDPIILDADIALIKLIDKARIST 574
DB 820 IDPSQFKIYLGKFRYDDDDREKTIQSLQISAILHBNYDPIILDADIALIKLIDKARIST 574
QY 575 RVOPICLAASRDLSFQESHITVAGMNVLAADVSPGFKNIDTLRSQVSVSDSLC 630
DB 880 RVOPICLP--DIT--RHLKSGTLAAVYTGW---LNENNTYSEMIQAVLPVVAAS 930
QY 629 LCEOEHDHGIPVSTDMNFCASWEPTASDICTAETGIAAVSPFGRASPEPRHMLGL 688
DB 931 TCEEGYKADLPLTVIENMFCAQYK--KGRYDACSQSGG--PLVFADDSRTERRWLLEGI 987
QY 689 VMSYDKTCSH-RLSTAFTKVLFPKDMIER 717
```

Db 988 VSWGSPSGCGKANQYGGFTKVNFLSWIRQ 1017

RESULT 14

US-08-296-014A-4
Sequence 4, Application US/08296014A

Patent No. 5716834

GENERAL INFORMATION:

APPLICANT: Ding, Jeak Ling

APPLICANT: Ho, Bow

TITLE OF INVENTION: The Cloned Factor C cDNA of the

TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscopus

TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolaach & Birch

STREET: 810 Gatehouse Road, Suite 500 East

CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 22042

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/296.014A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy, Jr., Gerald M.

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1781-105P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

TELEX: 248345

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1019 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-296-014A-4

Query Match 16.9%; Score 665; DB 1; Length 1019;

Best Local Similarity .25.4%; Pred. No. 1.9e-46;

Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAEWNIMCRBCECYDIECYCPGKRE-----VVGTYTPCCRNENEDSCLIH 82

Db 184 PNGGWSNPPKPCIR---ECAMVSSPEHGKVNALSGDMIGATL-----RFSDDS--- 229

QY 83 PGCTIFENCKSCR-NGSMWGTL-----VVGTYTPCCRNENEDSCLIH 103

Db 230 PYVILIGETLTCCGNGKNGNGIIPQCKNLVPCRPDLDPVNAHAKYKIGVEQYKGPQGT 289

QY 104 -----DFYVKGFGYCAECR--AGWYCG--DCMR-----CGQVLR-- 133

Db 290 VTYTCSNRYFLMGDPLKCNPDGSMGSGQSPSCVKADEVDSDSKAVDFLDVGEPRVRIH 349

QY 134 APKGQILLES-----YPLNHCWETIHA-----KRGFVL----- 162

Db 350 CPACGSLTAGTGWGTATYIHELISVCPRAIHAGKLPNSGGAHVANNNGPYSDFLSLNGI 409

QY 163 ---QLREVMLSLEEDYM-----CQYDVEYRD-----GNNRQQLIKRYCGN--E 202

Db 410 KSELKSLIARFRRDYRSTAGSKSGCGPDGWFVENDCVVYTSKRAMERAQGVCTNMAA 469

QY 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

Db 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

QY 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

Db 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

QY 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

Db 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

QY 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

Db 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

QY 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

Db 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

QY 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

Db 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

QY 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

Db 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

QY 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

Db 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

QY 203 RPAPIQS--IGSSLHVLPHSDG--SKNPDGPH-----ALYEITTAQSS 241

Db 470 RLAVLDKVIYNSLTETLRGKGLTTTWIGLHRLDAEKPIWELMDRSNVVLNDLTFMAS 529

QY 242 SPCEHDTQCVL-----DKAGS-YKCACTAGYTGRCENTLLEERN---CSPDGGVNGYOKI 293

Db 530 GERGETNCVYMDIQDQLOSVMKTKSCFPQSSPACMDLSDRKAACDDPGLSLENGHATL 589

QY 294 TGGPGLINGRHAHAKIGTVASFPCNSYVLSGNEKRTCCQNGEMSGKOPIC--ACREPKI 351

Db 590 HGQS--IDGFYA--GGSIRYSCVHLHYLSTGETVCTTGTNGTWSAPRRCIKVITQNPV 645

QY 352 SDLVRRRVLPVQVQSETEPLHQLYSAFSPKQKQ---SAPYKPRALPFD----- 398

Db 646 PSYGSVEIKP---PSRTNSISRVGSPFLRLPRLPLAARAKPPRPSQSPSTVLASK 702

QY 399 --LPMGYOHLTOLOECISPFYRRGSSRRCTCRGKXSGRASCIPICIKIENTAP- 455

Db 703 VKLPBGHYRGSAIYTCESRYELLGSGQRCDNSGNMGRASCIPVCGRSDSRSP 762

QY 456 ----KTQGLRWPQALYRRTSGVHDGSLHKGMFLVCSGALVNERTVVAACVTDLG 510

Db 763 INGNSTELGOWPMQAGISRWLA-----DHNMFLOGGSLNEMKMITTAHCTYLSA 815

QY 511 KTMITKADLKVVLGKFRYDDDEKTIQSLQISAILHPNVDPIILDADIALKLIDRA 570

Db 816 TAEIIDPNQFKMYLGYKRRDSDDDYQVREALETHVNPNDPGMLNFDIALIOLKTPV 875

QY 571 RISTRVOPICLAASRLDSTSFQESH-----TVAGMNVLADVRSPGKNDLTRGSVSY 624

Db 876 TLTRVOPICLPT--DITT---REHLKEGTLAVVTG---LNENNTSETIQOAVLPV 926

QY 625 VDSLCEOEHDHGIPVSYTDNMFCASWEPTASDICTAETGIAAVSPGRASPEPRMH 684

Db 927 VAASTCEGYKEADPLVTENMFCAGYK-KGRYDACSGBSGG--PLVFADSRTERRW 963

QY 685 LMLVSKSYKTCSH-RLSTAFTKVLPRKDWIR 717

Db 984 LEGIVSWSPSGCGKANQYGGFTKVNFLSWIRQ 1017

QY 984 LEGIVSWSPSGCGKANQYGGFTKVNFLSWIRQ 1017

Db 984 LEGIVSWSPSGCGKANQYGGFTKVNFLSWIRQ 1017

QY 984 LEGIVSWSPSGCGKANQYGGFTKVNFLSWIRQ 1017

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Db 984 LEGIVSWSPSGCGKANQYGGFTKVNFLSWIRQ 1017

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Db 984 LEGIVSWSPSGCGKANQYGGFTKVNFLSWIRQ 1017

QY 984 LEGIVSWSPSGCGKANQYGGFTKVNFLSWIRQ 1017

Db 984 LEGIVSWSPSGCGKANQYGGFTKVNFLSWIRQ 1017

QY 984 LEGIVSWSPSGCGKANQYGGFTKVNFLSWIRQ 1017

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GenCore version 6.2
Copyright (c) 1993 - 2007 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2007, 21:56:36 ; Search time 22 Seconds
(without alignments)
3148.912 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945

Sequence: 1 MEIGCWTQGLTFLOLLIS.....LSNATFKVLPRKQWIRNNK 720

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621563 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	949	24.1	181	2 T08805	hypothetical prote
2	672	17.0	1019	2 A38738	coagulation factor
3	482	12.2	699	1 I54763	Ra-reactive factor
4	403.5	10.2	705	1 C1HURB	complement subcomp
5	400.5	10.2	686	1 A59271	Ra-reactive factor
6	378.5	9.6	695	1 S05008	complement subcomp
7	354	9.0	1524	2 J30337	polyprotein - Afri
8	340.5	8.6	694	2 J06554	complement subcomp
9	334	8.5	688	1 C1HUS	complement subcomp
10	331.5	8.4	1019	1 A56318	enteropeptidase (E
11	330.5	8.4	1034	1 A53663	enteropeptidase (E
12	320	8.1	461	1 UX0210	protein C (activat
13	317.5	8.0	1035	1 A43090	enteropeptidase (E
14	314.5	7.9	855	1 EXCH	coagulation factor
15	313	7.9	855	2 J07731	membrane-bound arg
16	310.5	7.9	441	1 KKHU	protein C (activat
17	299.5	7.6	443	2 I46932	coagulation factor
18	293.5	7.4	407	1 KFB07	coagulation factor
19	292	7.4	461	1 S18994	protein C (activat
20	285.5	7.2	452	1 A30351	coagulation factor
21	283.5	7.1	482	1 EXRT	coagulation factor
22	282	7.1	456	1 KXBO	coagulation factor
23	281.5	7.1	558	1 J05878	plasma hyaluronan
24	281	7.1	492	1 EXBO	coagulation factor
25	280.5	7.1	264	2 I38136	chymotrypsin-like
26	280	7.1	562	1 UKHUT	t-plasminogen acti
27	278.5	7.0	466	1 KFHU7	coagulation factor
28	278	7.0	488	1 EXHU	coagulation factor
29	276	7.0	1113	2 J00315	low-density lipopr

30	277	7.0	559	1 A29941	t-plasminogen acti
31	277	7.0	559	1 A35029	t-plasminogen acti
32	276.5	7.0	625	1 A46688	hepatocyte growth
33	274.5	7.0	625	1 TBBO	thrombin (EC 3.4.2
34	273	6.9	560	1 JC4795	plasma hyaluronan
35	270	6.8	477	2 J05097	t-plasminogen acti
36	264.5	6.7	431	2 J05099	t-plasminogen acti
37	264.5	6.7	618	2 A35827	thrombin (EC 3.4.2
38	262.5	6.7	461	1 KFHU	coagulation factor
39	262	6.6	477	2 J05098	t-plasminogen acti
40	261.5	6.6	442	1 UKPE	u-plasminogen acti
41	261	6.6	431	1 UKHU	u-plasminogen acti
42	261	6.6	433	1 JN0560	u-plasminogen acti
43	260	6.6	477	1 A34369	t-plasminogen acti
44	259	6.6	244	2 S72219	chymotrypsin B - A
45	259	6.6	416	1 KFB0	coagulation factor
46	258.5	6.6	786	1 A47547	serine proteinase
47	258	6.5	251	2 PC1235	29K serine protein
48	258	6.5	433	1 UKGAY	u-plasminogen acti
49	257.5	6.5	1004	2 T30338	ovibactin (EC 3.4.
50	255.5	6.5	763	2 T50807	complement factor
51	254	6.4	617	2 S10511	thrombin (EC 3.4.2
52	253	6.4	1070	2 T31069	collid-BMP-1 like
53	249.5	6.3	400	1 A48050	coagulation factor
54	249.5	6.3	459	2 J00419	coagulation factor
55	248.5	6.3	263	1 B58788	coagulation factor
56	248	6.3	638	1 A31299	chymotrypsin (EC 3
57	248	6.3	991	2 K0HUP	plasma kallikrein
58	247.5	6.3	991	2 I49540	procollagen C-endo
59	247	6.3	275	2 A32410	trypsinase (EC 3.4.2
60	247	6.3	764	1 BHHU	complement factor
61	246.5	6.2	347	1 G00006	haploglobin - blac
62	246.5	6.2	622	1 TBHU	thrombin (EC 3.4.2
63	246	6.2	236	2 C42696	thrombin (EC 3.4.2
64	246	6.2	812	1 PLBO	thrombin (EC 3.4.2
65	245	6.2	234	2 F42696	plasma kallikrein
66	244	6.1	638	1 K0WSP	procollagen C-endo
67	242.5	6.1	730	1 BHHU1	trypsin (EC 3.4.21
68	241.5	6.1	823	1 A58788	trypsin (EC 3.4.21
69	240	6.1	242	2 S49489	haploglobin precu
70	239.5	6.1	406	1 HPHU2	chymotrypsin (EC 3
71	239	6.1	245	1 KYBOA	trypsin (EC 3.4.21
72	238	6.0	237	1 TRCY1	trypsin (EC 3.4.21
73	238	6.0	263	2 A21195	chymotrypsin (EC 3
74	238	6.0	347	1 HPHU1	haploglobin precu
75	238	6.0	375	1 A23689	limulus clotting e
76	237.5	6.0	810	2 I46260	plasma (EC 3.4.21
77	237	6.0	263	1 KYRBA	chymotrypsin (EC 3
78	236.5	6.0	274	2 J04171	trypsin (EC 3.4.2
79	236.5	6.0	707	2 J02218	procollagen C-endo
80	235	6.0	270	2 S56160	mast cell trypsinase
81	235	6.0	345	2 I36941	haploglobin - chim
82	235	6.0	1420	2 A32869	apolipoprotein(a)
83	233.5	5.9	263	2 S47537	chymotrypsin (EC 3
84	232	5.9	416	1 S33777	hepsin (EC 3.4.21
85	232	5.9	638	1 KQRP	plasma kallikrein
86	229.5	5.8	329	1 HPDG	haploglobin precu
87	228.5	5.8	235	2 E42696	thrombin (EC 3.4.2
88	228.5	5.8	347	1 HPMS	haploglobin precu
89	228.5	5.8	861	2 A48825	Notch homolog Motc
90	228.5	5.8	2531	2 A46019	notch-1 protein -
91	228	5.8	812	1 PLMS	plasma (EC 3.4.21
92	227.5	5.8	242	2 S31775	trypsin (EC 3.4.21
93	227.5	5.8	349	2 I36944	haploglobin - chim
94	227	5.8	242	2 S31776	trypsin (EC 3.4.21
95	227	5.8	1464	2 S58984	development protei
96	226.5	5.7	228	2 S31779	trypsin (EC 3.4.21
97	226.5	5.7	761	2 J05759	brain-specific ser
98	226	5.7	394	2 UC5060	t-plasminogen acti
99	226	5.7	625	1 KFHU1	coagulation factor
100	225	5.7	615	1 KFHU12	coagulation factor
101	224.5	5.7	271	1 ELRT2	pancreatic elastase
102	224	5.7	245	1 KYBOB	chymotrypsin (EC 3

103	223.5	5.7	274	2	S35339	176	199.5	5.1	2555	2	A40043	notch protein homo
104	223.5	5.7	348	1	HPHUR	177	198.5	5.0	229	1	TRBOTR	trypsin (EC 3.4.21
105	222.5	5.6	417	1	S00845	178	198.5	5.0	232	1	KOPG	tissue kallikrein
106	222.5	5.6	434	1	A35005	179	198.5	5.0	237	2	S55378	serine proteinase
107	222.5	5.6	790	1	PLPG	180	198	5.0	229	2	S68424	allergen Der f III
108	222	5.6	269	2	A26823	181	198	5.0	270	2	B29334	pancreatic elastas
109	222	5.6	275	2	S18583	182	198	5.0	760	1	C2MS	classical-compleme
110	221.5	5.6	2531	2	B35863	183	197.5	5.0	250	2	T01779	trypsin (EC 3.4.21
111	221	5.6	274	2	S31778	184	197.5	5.0	258	2	I36947	haptoglobin Hpp -
112	220.5	5.6	274	2	A45754	185	196.5	5.0	259	2	C26823	pancreatic elastas
113	220.5	5.6	1057	1	A39288	186	196.5	5.0	570	2	A48836	fibropellin C prec
114	220	5.6	275	2	A35863	187	196.5	5.0	767	2	T35018	hypothetical prote
115	219.5	5.6	235	2	H42696	188	196.5	5.0	2524	2	A35844	xotch protein - Af
116	219.5	5.6	271	2	A25528	189	196	5.0	3623	2	T08618	intrinsic factor-B
117	219.5	5.6	761	1	BIMS	190	195.5	5.0	271	2	I46580	factor IX - pig (f
118	219	5.6	343	1	A57014	191	195	4.9	432	1	S18932	u-plasminogen acti
119	218	5.5	271	2	S41308	192	194.5	4.9	246	1	TRRT1	trypsin (EC 3.4.21
120	217.5	5.5	243	2	A56338	193	194	4.9	261	2	A25606	tissue kallikrein
121	217	5.5	239	2	A27207	194	194	4.9	267	2	S40006	trypsin (EC 3.4.21
122	217	5.5	268	2	S68825	195	193.5	4.9	229	2	A55634	granzyme M (EC 3.4
123	217	5.5	273	2	A47246	196	193.5	4.9	347	1	HPPR	haptoglobin precur
124	217	5.5	603	2	S28941	197	193.5	4.9	2471	2	A49128	cell fate determin
125	217	5.5	2703	1	A24420	198	193	4.9	240	1	CPBOA3	procarboxypeptidas
126	216.5	5.5	236	2	I42696	199	193	4.9	246	1	DBHU	complement factor
127	216.5	5.5	346	2	I36942	200	191.5	4.9	247	1	A25852	trypsin (EC 3.4.21
128	216.5	5.5	2616	2	A57096	201	191.5	4.9	281	2	T13596	trypsin homolog -
129	216	5.5	810	1	PLHU	202	191.5	4.9	830	2	A30359	P-selectin precurs
130	215.5	5.5	248	2	TRDG	203	190.5	4.8	579	2	UC7629	membrane-type friz
131	215.5	5.5	248	2	S55066	204	190.5	4.8	579	2	A42755	P-selectin precurs
132	215	5.4	241	2	S39048	205	190.5	4.8	1064	2	A40136	fibropellin Ia - s
133	215	5.4	268	2	S68826	206	189.5	4.8	266	2	S54146	trypsin (EC 3.4.21
134	214.5	5.4	247	2	S13813	207	189.5	4.8	1737	2	T00209	MEGF8 protein - hu
135	214.5	5.4	366	2	JE0105	208	189	4.8	246	2	JQ1472	trypsin (EC 3.4.21
136	214.5	5.4	593	2	S45281	209	189	4.8	247	2	S05494	trypsin (EC 3.4.21
137	214	5.4	275	2	C35863	210	189	4.8	253	2	A53968	serine proteinase
138	213.5	5.4	235	2	D42696	211	189	4.8	258	4	S70439	pancreatic elastas
139	213.5	5.4	2352	2	I30201	212	189	4.8	267	4	A56615	probable pancreati
140	212	5.4	460	2	I56559	213	189	4.8	646	2	JN0473	P-selectin precurs
141	212	5.4	455	2	A61545	214	188.5	4.8	282	2	I46421	coagulation factor
142	211	5.3	237	2	S68702	215	188	4.8	253	2	S15686	tissue kallikrein
143	211	5.3	276	2	A38654	216	187.5	4.8	250	2	S55493	serine proteinase
144	210.5	5.3	1220	2	A56156	217	187.5	4.8	259	2	I38363	trypsin (EC 3.4.21
145	210	5.3	2437	2	S42612	218	187.5	4.8	304	2	S33496	trypsin (EC 3.4.21
146	209	5.3	433	1	UKMS	219	187	4.7	246	2	JQ1471	trypsin (EC 3.4.21
147	208.5	5.3	258	2	I36945	220	187	4.7	261	2	S45303	tissue kallikrein
148	207.5	5.3	239	2	G42696	221	187	4.7	271	2	S29239	chymotrypsin (EC 3
149	207.5	5.3	269	2	B26823	222	186	4.7	1594	2	T30549	hensin - rabbit
150	207	5.2	238	1	TRKVSY	223	185.5	4.7	711	1	A47136	macrophage-stimula
151	206.5	5.2	246	1	TRRT2	224	185.5	4.7	927	1	JQ0948	A5 antigen precurs
152	206.5	5.2	256	2	T10109	225	185	4.7	256	1	NGMSA	7S nerve growth fa
153	206	5.2	430	1	A24702	226	183.5	4.7	1372	2	T25933	hypothetical prote
154	206	5.2	4548	1	S00657	227	183	4.6	265	1	KQRTP	tissue kallikrein
155	205.5	5.2	269	2	B32410	228	183	4.6	392	1	A30100	serine proteinase
156	205.5	5.2	460	2	B61545	229	182.5	4.6	482	2	JC5092	E-selectin - pig
157	204.5	5.2	367	2	JE0104	230	182.5	4.6	722	2	I48324	DELTA-like 1 - mou
158	204.5	5.2	752	1	C2HU	231	182.5	4.6	2531	2	T31070	notch homolog - se
159	204.5	5.2	1203	2	A49175	232	182	4.6	261	1	TRMSMS	tissue kallikrein
160	203.5	5.2	247	1	B25852	233	181.3	4.6	247	1	PRMSCL	granzyme B (EC 3.4
161	203.5	5.2	263	1	I55608	234	181.5	4.6	247	2	S12764	trypsin (EC 3.4.21
162	203.5	5.2	285	2	I48144	235	181.5	4.6	258	2	A45161	serine proteinase
163	203.5	5.2	309	2	B49878	236	181.5	4.6	437	2	S18407	acrosin (EC 3.4.21
164	203.5	5.2	3623	2	T09456	237	181	4.6	261	1	NGMSG	7S nerve growth fa
165	203	5.1	403	2	C82228	238	181	4.6	418	2	A37344	acrosin (EC 3.4.21
166	202	5.1	240	2	S39047	239	181	4.6	1291	2	T21694	hypothetical prote
167	202	5.1	2321	2	S78549	240	180.5	4.6	248	2	S55067	trypsin (EC 3.4.21
168	201.5	5.1	246	2	B25528	241	180.5	4.6	275	2	I46712	factor IX - rabbit
169	200.5	5.1	226	1	KCUF	242	180.5	4.6	436	2	JX0172	acrosin (EC 3.4.21
170	200.5	5.1	231	1	TRPGR	243	180	4.6	254	2	S49329	trypsin-like prote
171	200.5	5.1	810	2	B30848	244	180	4.6	261	2	S01971	tissue kallikrein
172	199.5	5.1	247	2	A27547	245	180	4.6	275	2	S40005	trypsin (EC 3.4.21
173	199.5	5.1	257	2	S33772	246	179.5	4.6	243	2	A35871	trypsin (EC 3.4.21
174	199.5	5.1	258	2	G02959	247	179.5	4.6	259	1	WMMS28	complement factor
175	199.5	5.1	275	2	S40007	248	179.5	4.6	274	2	I47078	coagulation factor

249	179.5	4.6	728	2	I50719	C-Delta-1 - chicke	322	161.5	4.1	250	2	S31384	trypsin (EC 3.4.21
250	179.5	4.6	1047	2	A55617	pancreatic precurs	323	161.5	4.1	261	2	S40162	cathepsin G (EC 3.
251	179	4.5	266	1	ELRG	pancreatic elastas	324	161.5	4.1	265	2	T15451	hypothetical prote
252	179	4.5	612	2	B42755	E-selectin precurs	325	161.5	4.1	832	2	A31246	neurogenic protein
253	178.5	4.5	402	2	UH0403	procollagen I C-pr	326	161.5	4.1	880	2	S00670	neurogenic protein
254	177.5	4.5	248	2	A43520	natural killer cel	327	161.5	4.1	1025	1	A43526	complement C3d/Eps
255	177.5	4.5	420	2	A55283	acrosin (EC 3.4.21	328	161	4.1	1827	2	T34288	hypothetical prote
256	177.5	4.5	1964	2	T09059	notch4 - mouse	329	160.5	4.1	661	1	KRHU13	hypothetical prote
257	177	4.5	268	2	UQ1473	pancreatic elastas	330	160	4.1	262	1	A31372	coagulation factor
258	177	4.5	473	2	A56175	adhesive plaque pr	331	160	4.1	3002	2	A47221	granzyme A (EC 3.4
259	177	4.5	747	2	I51579	complement factor	332	159.5	4.0	1722	2	E89753	fibrillin 1 precu
260	176.5	4.5	1091	1	PL0009	complement C3d/Eps	333	159	4.0	244	2	A44284	protein FltC7.4 (l
261	176	4.5	261	2	A29745	cissue kallikrein	334	159	4.0	261	2	A28062	cissue kallikrein
262	176	4.5	261	2	A31136	cissue kallikrein	335	159	4.0	2907	2	A57278	gamma-tenin (EC 3.
263	176	4.5	264	2	S32794	trypsin-like prote	336	158.5	4.0	2907	2	A57278	fibrillin-2 precu
264	176	4.5	2318	2	S45306	notch 3 protein -	337	158.5	4.0	247	2	S59135	maet cell proteina
265	175.5	4.4	274	2	S40004	trypsin-related pr	338	158.5	4.0	833	2	S19087	homeotic protein d
266	175	4.4	270	2	A29934	pancreatic elastas	339	158	4.0	610	2	T16761	gene Delta protein
267	175	4.4	421	1	S11674	acrosin (EC 3.4.21	340	158	4.0	2918	2	A54105	hypothetical prote
268	174.5	4.4	232	2	S32398	serine proteinase	341	157.5	4.0	579	2	A54105	fibrillin-2 precu
269	174.5	4.4	246	1	TRDGC	trypsin (EC 3.4.21	342	157.5	4.0	507	2	A56740	sperm-egg recognit
270	174	4.4	259	2	A29746	cissue kallikrein	343	157	4.0	261	2	T27317	hypothetical prote
271	174	4.4	261	1	KQMS1	cissue kallikrein	344	157	4.0	610	2	A35046	cissue kallikrein
272	174	4.4	1295	2	A32901	g1p1 protein precu	345	156.5	4.0	252	2	A36172	E-selectin precurs
273	173.5	4.4	548	2	D82175	probable trypsin V	346	156.5	4.0	275	2	JC6506	procytotoxic T-lym
274	173	4.4	229	1	TRDPS	trypsin (EC 3.4.21	347	156.5	4.0	1429	2	S06434	tumor necrosis fac
275	173	4.4	768	2	I53821	P-selectin - fat	348	156.5	4.0	3635	2	T10053	homeotic protein l
276	172.5	4.4	248	1	PRMSC2	granzyme C (EC 3.4	349	156	4.0	259	2	KQRTN	laminin alpha 5 ch
277	172.5	4.4	277	2	S35340	trypsin (EC 3.4.21	350	156	4.0	262	2	A29586	tomn (EC 3.4.21.-
278	172.5	4.4	431	2	S47538	acrosin (EC 3.4.21	351	156	4.0	702	2	T16832	cissue kallikrein
279	172.5	4.4	449	2	A55362	procollagen I C-pr	352	155.5	3.9	213	2	S17537	hypothetical prote
280	172	4.4	254	2	S65465	trypsin-like prote	353	155.5	3.9	485	2	S36772	fibrynolytic prote
281	172	4.4	261	2	A24378	cissue kallikrein	354	155.5	3.9	533	2	JC7985	E-selectin - bov
282	172	4.4	250	1	A34170	acrosin (EC 3.4.21	355	155	3.9	250	2	S15685	brain-specific CUB
283	171.5	4.3	435	2	A27802	hypodermin C (EC 3	356	155	3.9	2489	2	I73012	kallikrein, glandu
284	171.5	4.3	262	1	KQHU	cissue kallikrein	357	154.5	3.9	659	2	A34877	complement C3b/C4b
285	171.5	4.3	2403	2	A59386	sanko - human	358	154	3.9	262	2	S65551	C4b-binding protei
286	171	4.3	257	2	B45061	granzyme A (EC 3.4	359	153.5	3.9	251	2	JC2125	factor H - bovine
287	171	4.3	260	2	A45061	granzyme A (EC 3.4	360	153.5	3.9	387	2	B49175	cinnase (EC 3.4.21
288	171	4.3	266	1	ELRT1	pancreatic elastas	361	153.5	3.9	551	2	I46709	Motch A protein -
289	171	4.3	273	2	S40003	trypsin-related pr	362	153.5	3.9	1786	1	MMMSB1	endothelial leukoc
290	171	4.3	2139	2	A35672	crumbs protein - f	363	153	3.9	152	2	A53274	laminin beta-1 cha
291	170	4.3	248	2	S33756	granzyme-like prote	364	153	3.9	254	1	TRWV3Y	complement factor
292	170	4.3	266	2	JC4850	trypsin-like prote	365	153	3.9	2871	2	A55567	trypsin-like prote
293	169.5	4.3	251	2	T10262	maet cell serine p	366	152.5	3.9	248	1	S01007	granzyme F (EC 3.4
294	169.5	4.3	261	1	S35711	semenogelase (EC 3	367	152.5	3.9	264	2	S65663	granzyme 3 (EC 3.4
295	169.5	4.3	421	2	S29599	acrosin (EC 3.4.21	368	152.5	3.9	385	2	A54785	preadipocyte facto
296	169.5	4.3	560	2	T16833	hypothetical prote	369	152.5	3.9	422	1	KXHUZ	plasma protein Z p
297	169	4.3	214	2	S17680	fibrynolytic prote	370	152	3.9	281	1	A61021	granzyme B (EC 3.4
298	169	4.3	246	2	S64707	chymase (EC 3.4.21	371	152	3.9	686	2	JC7569	Delta-4 protein -
299	169	4.3	259	2	B31136	cissue kallikrein	372	151.5	3.8	761	2	A34079	cissue kallikrein
300	169	4.3	504	2	S56745	mucin (clone pGM31	373	151.5	3.8	216	1	A40332	macrophage-stimula
301	168.5	4.3	248	2	S33755	granzyme-like prote	374	151.5	3.8	977	2	I52657	seizure-related pr
302	168	4.3	597	2	S71352	metalloproteinase	375	151.5	3.8	249	1	A35842	chymase (EC 3.4.21
303	168	4.3	2014	3	I36936	complement recepto	376	151	3.8	261	2	A41020	cissue kallikrein
304	167.5	4.2	261	1	A32297	semenogelase (EC 3	377	151	3.8	1620	2	T27283	hypothetical prote
305	167.5	4.2	383	2	S53716	delta-like homeoti	378	150.5	3.8	248	2	S43259	granzyme-like prote
306	167	4.2	247	2	S45113	granzyme-like prote	379	150.5	3.8	277	2	A41735	hyaluronate-bindin
307	167	4.2	260	2	A37938	cissue kallikrein	380	150.5	3.8	285	2	T35195	probable serine pr
308	166	4.2	265	2	T10495	chymotrypsin (EC 3	381	150.5	3.8	685	2	JC7570	Delta-4 protein -
309	165	4.2	2043	2	T18524	scavenger receptor	382	150.5	3.8	1053	2	S46199	probable complemen
310	164.5	4.2	449	1	NBHHS	complement factor	383	150	3.8	263	1	WMVZSP	apolipoprotein H h
311	164.5	4.2	1231	1	NBHHS	complement factor	384	150	3.8	267	1	ELRHL	leukocyte elastase
312	164	4.2	230	2	I48685	maet cell proteina	385	150	3.8	601	1	B36346	fibrillin 1 precu
313	164	4.2	613	2	S15468	complement C3b/C4b	386	150	3.8	770	2	T00203	LDL receptor-relat
314	164	4.2	2871	2	A55624	fibrillin-1 precu	387	150	3.8	3712	2	S18253	laminin alpha-1 ch
315	163	4.1	868	2	T20239	hypothetical prote	388	149.5	3.8	236	1	A32121	snake venom factor
316	162.5	4.1	276	2	A47290	TSG-6 homolog PS4	389	149.5	3.8	259	1	TRSMG	cissue kallikrein
317	162.5	4.1	1290	2	A57190	ednetin precursor	390	149.5	3.8	13288	2	T03099	mucin, submaxillar
318	162.5	4.1	2083	2	T42721	CRP-ductin-alpha p	391	149	3.8	216	1	KYVH20	chymotrypsin (EC 3
319	162	4.1	261	1	EGMSB	cissue kallikrein	392	149	3.8	683	2	C36346	fibrillin 1 precu
320	161.5	4.1	226	2	S69370	duodenase - bovine	393	149	3.8	770	2	T00204	LDL receptor relat
321	161.5	4.1	248	2	S01006	cytotoxic T-lympho	394	149	3.8	1408	2	S16148	gene serrate prote

395	148	3.8	218	1	KYV2C	chymotrypsin (EC 3	468	134	3.4	3034	2	T14119	seven-pass transme
396	148	3.8	668	2	A46013	coagulation factor	469	133.5	3.4	154	2	S35207	protease 7 - buf
397	148	3.8	1469	2	B36655	slit protein 2 pre	470	133.5	3.4	1687	2	T30176	EGF repeat transme
398	148	3.8	1480	2	A36655	slit protein 1 pre	471	133.5	3.4	3507	2	T34513	hypothetical prote
399	147.5	3.7	244	2	A46721	chymase (EC 3.4.21	472	133	3.4	810	2	T10756	Nel-homolog protei
400	147.5	3.7	244	2	A34910	mast cell proteina	473	132.5	3.4	331	2	T27906	hypothetical prote
401	147.5	3.7	597	1	S53711	C4BP alpha chain p	474	132	3.3	246	2	A38678	mast cell proteina
402	147.5	3.7	1786	1	MMHUB1	laminin beta-1 cha	475	132	3.3	372	2	JC5377	L-selectin precurs
403	147.5	3.7	4391	2	A38096	perlecan precursor	476	132	3.3	558	2	S57953	C4BP protein alpha
404	147	3.7	236	2	A28566	T-cell suppressor	477	132	3.3	2109	1	I50421	aggrecan precursor
405	147	3.7	259	2	D23863	ribase kallikrein	478	132	3.3	3871	2	T22812	hypothetical prote
406	147	3.7	262	1	JC4803	venombin A (EC 3.4	479	131.5	3.3	302	1	WMBB1E	secretory compleme
407	147	3.7	716	1	JC5061	macrophage-stimula	480	131.5	3.3	1268	2	S52781	neurocan - mouse
408	147	3.7	1557	2	T28811	hypothetical prote	481	130.5	3.3	1257	2	S28764	neurocan precursor
409	147	3.7	3084	1	MMMSA	laminin alpha-1 ch	482	130.5	3.3	3672	2	T23433	hypothetical prote
410	146.5	3.7	236	1	B32121	heparan sulfate fac	483	130.5	3.3	3704	2	T37316	probable laminin a
411	146.5	3.7	3707	2	S18252	hypothetical prote	484	129.5	3.3	233	1	JG0169	venombin A (EC 3.4
412	146	3.7	263	2	T28450	hypothetical prote	485	129.5	3.3	376	2	JC0492	decay-accelerating
413	145	3.7	256	1	TRPF	trypsin-like prote	486	129.5	3.3	381	1	B26359	decay-accelerating
414	145	3.7	263	1	C36838	L-selectin precurs	487	129.5	3.3	440	2	A26359	venombin AB (EC 3.
415	145	3.7	372	1	A32375	tenascin-like prot	488	129	3.3	235	1	S65621	cathepsin G (EC 3.
416	145	3.7	782	2	B16525	mast cell proteina	489	128.5	3.3	255	2	A27122	hypothetical prote
417	144.5	3.7	246	2	B38678	trypsin homolog -	490	128.5	3.3	321	2	T33161	azurocidin - pig
418	144.5	3.7	303	2	T13598	trypsin control	491	128	3.2	5147	1	JTRPAZ	cadherin-related c
419	144.5	3.7	360	2	T42921	trypsin homolog -	492	128	3.2	1531	2	T42218	slit-1 protein hom
420	144	3.7	685	2	B78040	fibulin, splice fo	493	127.5	3.2	258	2	I56220	trypsinase 2 - rat
421	144	3.7	263	2	B7152	chymase (EC 3.4.21	494	127	3.2	1609	1	MMHUB2	laminin gamma-1 ch
422	143.5	3.6	247	2	S23504	chymase (EC 3.4.21	495	127	3.2	1751	1	MMHOMH	laminin alpha-2 ch
423	143	3.6	3075	2	S14458	chymase (EC 3.4.21	496	127	3.2	3106	1	S53868	laminin alpha-2 ch
424	142.5	3.6	260	2	S26403	trypsin-like prote	497	127	3.2	1025	2	T42626	secreted leucine-r
425	142	3.6	272	2	JC4170	metalloproteinase	498	126.5	3.2	265	2	A38894	serine proteinase
426	141.5	3.6	310	2	S41055	L-selectin precurs	499	126	3.2	265	2	J50260	serine proteinase
427	141.5	3.6	385	1	A34015	probable serine pr	500	126	3.2	265	2	I56100	complement factor
428	141	3.6	225	2	S45356	cytotoxic T-lympho	501	126	3.2	642	2	S53433	plasma protein S p
429	141	3.6	246	2	A32692	chymase (EC 3.4.21	502	126	3.2	254	2	S35585	chymotrypsin-like
430	140.5	3.6	246	1	A6504	complement factor	503	125.5	3.2	265	2	I48679	neutrophil elastase
431	140.5	3.6	1234	1	NBMSH	odt protein - frui	504	125.5	3.2	597	2	NBRUC4	C4b-binding protei
432	140.5	3.6	2406	2	A54148	tenascin-like prot	505	125.5	3.2	152	2	S35209	serine proteinase
433	140.5	3.6	2515	2	S47008	plasma protein Z -	506	125	3.2	323	1	S09702	L-selectin precurs
434	140	3.5	396	1	KXBOZ	chymotrypsin (EC 3	507	125	3.2	1790	1	MMFRB1	laminin beta-1 cha
435	139.5	3.5	258	1	S44184	hypothetical prote	508	125	3.2	548	2	A33412	cytotoxic T-lympho
436	139.5	3.5	288	2	T33224	UVS.2 protein - Af	509	124.5	3.2	248	2	T16642	hypothetical prote
437	139.5	3.5	319	2	I51569	latent transforin	510	124.5	3.2	330	2	T46256	brevican - human (
438	139	3.5	1820	2	A55494	chymase (EC 3.4.21	511	124	3.1	710	1	I51383	hepatocyte growth
439	138.5	3.5	244	2	S26042	fibulin, splice fo	512	124	3.1	883	2	S49126	brevican precursor
440	138.5	3.5	247	1	KYHUC	hypothetical prote	513	124	3.1	1221	2	A49457	MEGFs protein - ra
441	138.5	3.5	705	2	S34958	complement factor	514	124	3.1	1583	2	T13953	hypothetical prote
442	138.5	3.5	1111	2	T26972	complement factor	515	124	3.1	1584	2	T22674	hypothetical prote
443	137.5	3.5	191	2	S54115	C4BP protein beta	516	124	3.1	2180	2	T29764	proteinase 5 - buf
444	137.5	3.5	808	2	D35069	L-selectin precurs	517	124	3.1	151	2	S35205	chymotrypsin (EC 3
445	137	3.5	258	2	S57960	protein T22A3.8 [l	518	123.5	3.1	370	2	S49129	L-selectin precurs
446	137	3.5	372	2	S23936	hypothetical prote	519	123.5	3.1	699	2	T33375	hypothetical prote
447	137	3.5	2823	2	R87908	laminin alpha chai	520	123.5	3.1	1184	2	A55184	chymotrypsin (EC 3
448	137	3.5	2823	2	T33064	mast cell proteina	521	123.5	3.1	248	2	S49323	epidermal growth f
449	137	3.5	3102	2	T43291	cysteine rich prot	522	123.5	3.1	340	2	JC7125	decay-accelerating
450	136.5	3.5	247	1	PRRTG	membrane-bound com	523	123	3.1	798	2	T22793	hypothetical prote
451	136.5	3.5	1274	1	T42017	complement C3b rec	524	123	3.1	1955	1	AGCH	hypothetical prote
452	136	3.4	360	1	WMBB2E	MEGF6 protein - ra	525	123	3.1	2844	2	S288291	receptor tyrosine
453	136	3.4	676	2	A45900	laminin gamma-1 ch	526	123	3.1	1081	2	T31329	serine proteinase
454	136	3.4	1574	2	T13954	hypothetical prote	527	123	3.1	158	2	I46002	C4BP beta chain -
455	136	3.4	1607	1	MMMSB2	complement factor	528	122.5	3.1	676	1	KXHUS	plasma protein S p
456	135.5	3.4	226	2	JE0151	agglutinin factor	529	122	3.1	416	2	A48598	agrin precursor -
457	135.5	3.4	372	2	T29359	apoliipoprotein H p	530	122	3.1	245	2	T20448	kallikrein-like se
458	135.5	3.4	452	2	A35068	hypothetical prote	531	122	3.1	610	1	I46001	hypothetical prote
459	135.5	3.4	469	1	NBMS4	protein P40E10.4 [532	122	3.1	5376	2	T42215	C4b-binding protei
460	135	3.4	159	2	I84615	hypothetical prote	533	122	3.1	647	2	A43902	zonahesin - mouse
461	135	3.4	343	1	NBHU	venombin A (EC 3.4	534	121.5	3.1	1627	2	S65464	pregnancy-associat
462	135	3.4	345	1	DB9711	hypothetical prote	535	121.5	3.1	2409	1	A60979	versican precursor
463	135	3.4	3051	2	S42373	hypothetical prote	536	121.5	3.1				
464	134.5	3.4	601	2	T22025	hypothetical prote	537	121.5	3.1				
465	134.5	3.4	601	2	T22025	hypothetical prote	538	121	3.1				
466	134	3.4	232	1	A54361	hypothetical prote	539	121	3.1				
467	134	3.4	2824	2	T22759	hypothetical prote	540	121	3.1				

541	120.5	3.1	247	2	S64708	chymase (EC 3.4.21	614	112	2.8	228	1	S35689	venombin A (EC 3.4
542	120.5	3.1	252	2	T46247	hypothetical prote	615	112	2.8	918	2	JC4361	scavenger receptor
543	120.5	3.1	345	1	JN0465	apolipoprotein H p	616	112	2.8	1125	1	S57846	protein-tyrosine k
544	120.5	3.1	497	2	JC2054	complement regulat	617	112	2.8	1353	1	JH0675	restrictin precurs
545	120.5	3.1	669	2	S38819	plasma protein S -	618	112	2.8	1639	1	MMFFB2	laminin gamma-1 ch
546	120.5	3.1	712	2	T42760	fibulin, splice fo	619	112	2.8	3562	2	A47171	chondroitin sulfat
547	120.5	3.1	728	1	T42390	fibulin 1, splice	620	112	2.8	4307	2	T20721	hypothetical prote
548	120.5	3.1	728	1	A60185	hepatocyte growth	621	111.5	2.8	159	2	S35202	proteinase 2 - buf
549	120.5	3.1	1394	2	A35626	transforming growt	622	111.5	2.8	370	2	JC7592	spinal cord-deriv
550	120.5	3.0	1801	1	MMRTS	laminin beta-2 cha	623	111.5	2.8	651	2	T19477	hypothetical prote
551	120	3.0	257	1	JC2479	venombin B (EC 3.4	624	111.5	2.8	1328	2	T43060	agrin - electric r
552	120	3.0	363	1	AJ3900	complement C3d/Eps	625	111.5	2.8	1797	2	A55677	laminin beta-2 cha
553	120	3.0	493	2	JC5621	epidermal growth f	626	111.5	2.8	2019	1	JQ1322	tenascin precursor
554	120	3.0	589	2	T43210	fibulin-1D precurs	627	111.5	2.8	2531	2	T16743	hypothetical prote
555	120	3.0	912	2	A54423	brevican precursor	628	111.5	2.8	4351	2	T00252	MEG1 protein - ra
556	120	3.0	1548	2	S34583	serine proteinase	629	111	2.8	231	2	A60468	venombin A (EC 3.4
557	120	3.0	1643	2	T14274	versican precursor	630	111	2.8	915	2	T21773	hypothetical prote
558	120	3.0	2397	1	A55535	versican precursor	631	110.5	2.8	297	1	S20407	venombin A (EC 3.4
559	120	3.0	3381	2	T42389	coagulation factor	632	110.5	2.8	408	2	T22801	apolipoprotein H p
560	119.5	3.0	161	2	I48158	complement C3b/C4b	633	110.5	2.8	583	2	A29154	hypothetical prote
561	119.5	3.0	482	1	A34924	plasma protein S p	634	110.5	2.8	678	2	B48089	growth arrest-spec
562	119.5	3.0	675	1	KKBOS	hel protein - chic	635	110.5	2.8	692	2	T32980	hypothetical prote
563	119.5	3.0	835	2	JF0076	integumentary mucr	636	110.5	2.8	961	1	TSHUP4	chromospondin 4 p
564	119.5	3.0	1247	1	MMHUND	venom plasminogen	637	110.5	2.8	1217	1	EGMSMG	plexin 1 precursor
565	119.5	3.0	1506	2	T30886	growth potentiatin	638	110.5	2.8	1894	2	JC4980	hypothetical prote
566	119	3.0	258	2	A57290	hepatocyte growth	639	110	2.8	266	2	T19292	protein-tyrosine k
567	119	3.0	513	2	D88991	hepatocyte growth	640	110	2.8	1124	1	I58838	plexin - African c
568	118.5	3.0	674	1	I55476	apernadhesin AMN -	641	110	2.8	1905	2	S06176	cytotoxic T-lympho
569	118.5	3.0	728	1	AJ5644	neurogenic repetit	642	110	2.8	2215	2	T00348	LRI1 protein - mou
570	118.5	3.0	728	1	JH0579	hypothetical prote	643	109.5	2.8	2825	2	T14271	hypothetical prote
571	118	3.0	133	2	S21114	brevican precursor	644	109.5	2.8	236	1	A41456	venombin A (EC 3.4
572	118	3.0	196	2	T08808	tissue kallikrein	645	109	2.8	497	2	E70414	Doc4 protein, stre
573	118	3.0	293	2	B26637	hypothetical prote	646	109	2.8	1700	2	T30273	azurocidin precurs
574	118	3.0	838	2	T20125	hypothetical prote	647	109	2.8	2476	2	T20968	hypothetical prote
575	118	3.0	883	2	S57653	hypothetical prote	648	108.5	2.8	2610	1	A41456	venombin A (EC 3.4
576	117.5	3.0	188	2	B32340	protein unc-52 [lm	649	108.5	2.7	251	1	TRHUZ2	hypothetical prote
577	117.5	3.0	259	2	T21011	protein unc-52 [lm	650	108	2.7	1450	2	T30273	hypothetical prote
578	117.5	3.0	642	2	SS3434	protein unc-52 [lm	651	108	2.7	1700	2	S08167	hypothetical prote
579	117.5	3.0	966	2	JM0237	protein unc-52 [lm	652	108	2.7	2476	2	T34022	hypothetical prote
580	117.5	3.0	1160	2	F88369	protein unc-52 [lm	653	108	2.7	640	2	T19346	hypothetical prote
581	117.5	3.0	2295	2	C88369	protein unc-52 [lm	654	107.5	2.7	670	2	I65967	hypothetical prote
582	117.5	3.0	3375	2	T19821	proteinase 3 (EC 3	655	107.5	2.7	3566	1	A40701	tenascin-X precurs
583	116.5	3.0	256	1	PRHU3	membrane cofactor	656	107.5	2.7	4544	1	S02392	alpha-2-macroglobu
584	116.5	3.0	377	2	I54479	Wnt inhibitory fac	657	107.5	2.7	280	1	G02741	skeletal muscle LI
585	116.5	3.0	378	2	B59180	membrane cofactor	658	107	2.7	497	2	T27827	hypothetical prote
586	116.5	3.0	384	2	S01896	laminin Blk chain	659	106.5	2.7	192	2	E70414	hypothetical prote
587	116.5	3.0	1170	2	A53612	osteonidogen - hum	660	106.5	2.7	362	2	JC5194	hypothetical prote
588	116	2.9	1376	2	G00043	complement recepto	661	106.5	2.7	369	2	JC5138	hypothetical prote
589	115.5	2.9	440	2	A43519	protein ZC84.6 [lm	662	106.5	2.7	616	2	T29234	hypothetical prote
590	115.5	2.9	1474	2	D88550	furin (EC 3.4.21.7	663	106.5	2.7	755	2	A44315	hypothetical prote
591	115.5	2.9	1680	2	A43434	ILM protein, FHL4	664	106.5	2.7	417	2	T33376	hypothetical prote
592	115	2.9	279	2	JG0164	epidermal growth f	665	106	2.7	657	2	T00859	hypothetical prote
593	115	2.9	1207	1	EGHU	complement factor	666	106	2.7	927	2	T21772	epidermal growth f
594	114.5	2.9	270	2	I37278	sperm CD46 - human	667	106	2.7	1133	1	EGRT	hypothetical prote
595	114.5	2.9	349	2	G02913	membrane cofactor	668	106	2.7	1142	2	T30272	hypothetical prote
596	114.5	2.9	369	2	I57998	laminin beta-2 cha	669	106	2.7	1522	2	H88380	protein T22F7.3 [l
597	114.5	2.9	369	2	S53869	venombin A (EC 3.4	670	106	2.7	1805	2	T21888	hypothetical prote
598	114	2.9	255	1	A28169	integrin beta chat	671	106	2.7	2195	2	T34264	hypothetical prote
599	114	2.9	741	2	T46488	hypothetical prote	672	105.5	2.7	596	2	T46914	hypothetical prote
600	114	2.9	846	2	A30889	hypothetical prote	673	105.5	2.7	673	2	A45664	variant-specific s
601	114	2.9	1069	2	T42681	hypothetical prote	674	105.5	2.7	860	1	A48089	growth arrest-spec
602	113.5	2.9	502	2	T22919	hypothetical prote	675	105.5	2.7	1107	2	T15884	LDL receptor precu
603	113.5	2.9	558	2	T17324	hypothetical prote	676	105	2.7	1746	1	S19694	tenascin precursor
604	113.5	2.9	574	2	B88465	protein B0244.8 [l	677	105	2.7	2201	2	A32160	tenascin-C - human
605	113.5	2.9	879	1	ORRTUD	LDL receptor precu	678	105	2.7	345	1	NBMS	apolipoprotein H p
606	113.5	2.9	1712	2	A38261	masking protein pr	679	104.5	2.6	1360	2	T33922	apolipoprotein H p
607	113.5	2.9	161	2	I62744	pancreatic elasta	680	104.5	2.6	345	1	NBBO	apolipoprotein H p
608	112.5	2.9	264	2	A28942	spinal cord-deriv	681	104	2.6	360	1	A55198	transcription fact
609	112.5	2.9	370	2	JC7591	trophozoite cytel	682	104	2.6	473	2	A59180	Wnt inhibitory fac
610	112.5	2.9	677	2	C42125	multimerin, endoth	683	104	2.6	2101	2	S57245	hypothetical prote
611	112.5	2.9	1228	2	A57384	hypothetical prote	684	104	2.6				
612	112.5	2.9	1797	2	T21889		685	104	2.6				
613	112.5	2.9					686	104	2.6				

687	104	2.6	4135	2	T42629	760	98	2.5	102	2	B55885	chondroitin sulfat
688	103.5	2.6	383	2	T21946	761	98	2.5	357	2	S23403	sperm surface prot
689	103	2.6	331	2	A45292	762	98	2.5	909	1	ORXLL1	LDL receptor 1 pre
690	103	2.6	412	2	S72579	763	98	2.5	937	2	I53282	gene PACB4 protein
691	103	2.6	1296	2	T16859	764	98	2.5	1087	2	T31100	probable potastium
692	103	2.6	2148	1	A56081	765	98	2.5	1748	1	UN0786	integrin beta-4 ch
693	102.5	2.6	153	2	S35204	766	98	2.5	2588	1	T14342	NSD1 protein - mou
694	102.5	2.6	473	2	I49283	767	98	2.5	4660	2	T42737	GP130 protein prec
695	102.5	2.6	565	2	T16408	768	97.5	2.5	577	2	A60501	thrombospondin pre
696	102.5	2.6	873	1	ORRBVD	769	97.5	2.5	837	1	A29512	LDL receptor precu
697	102	2.6	149	2	S35208	770	97.5	2.5	878	2	B71460	probable outer mem
698	102	2.6	280	2	G01884	771	97.5	2.5	884	2	T18649	hypothetical prote
699	102	2.6	380	2	G01639	772	97.5	2.5	1162	2	T21557	hypothetical prote
700	102	2.6	411	2	D88087	773	97.5	2.5	2946	2	T15840	hypothetical prote
701	102	2.6	718	2	T29448	774	97	2.5	126	2	A23473	chymotrypsin-like
702	102	2.6	863	1	S51789	775	97	2.5	379	2	T27350	hypothetical prote
703	102	2.6	1168	2	I56985	776	97	2.5	429	2	T21113	hypothetical prote
704	102	2.6	1713	2	A55347	777	97	2.5	626	2	T27319	hypothetical prote
705	102	2.6	4006	2	T09070	778	97	2.5	799	1	IUMGFB	fibronectin recept
706	101.5	2.6	379	2	T16213	779	97	2.5	808	2	T23129	hypothetical prote
707	101.5	2.6	1106	2	T18739	780	97	2.5	862	2	S43922	versican - pig-tai
708	101.5	2.6	1959	1	AGRT	781	97	2.5	935	1	A48225	subtilisin-like pr
709	101.5	2.6	2415	1	A59086	782	97	2.5	1138	1	S24066	protein-tyrosine k
710	101	2.6	377	2	C88710	783	97	2.5	1132	2	A44018	laminin B2t chain
711	101	2.6	463	2	T26655	784	97	2.5	1292	2	T09229	galactose binding
712	101	2.6	557	2	A48434	785	96.5	2.4	149	1	KQSM	tissue kallikrein
713	101	2.6	1371	2	A33837	786	96.5	2.4	317	2	D42526	BSR protein - vacc
714	101	2.6	1378	1	A648751	787	96.5	2.4	613	2	A69835	thrombospondin 3 p
715	101	2.6	1875	2	T24251	788	96.5	2.4	956	2	A57121	MI30 antigen precu
716	100.5	2.6	417	2	T20199	789	96.5	2.4	1149	2	T38006	hypothetical prote
717	100.5	2.5	670	2	S77463	790	96.5	2.4	1193	2	T21133	proteolitaisin - se
718	100.5	2.5	802	2	T24293	791	96.5	2.4	1297	2	T30274	hemocytin - saliko
719	100.5	2.5	949	2	T24294	792	96.5	2.4	3133	2	S52093	ACN-3 protein - pi
720	100.5	2.5	956	1	A46016	793	96	2.4	116	2	S17567	spermadhesin AQN-3
721	100.5	2.5	1252	2	S36016	794	96	2.4	116	2	S39434	crysin-related pr
722	100	2.5	1356	2	A45445	795	96	2.4	256	2	A56593	hypothetical prote
723	100	2.5	152	2	S35203	796	96	2.4	322	2	T25213	integrin beta-1* c
724	100	2.5	421	2	T25383	797	96	2.4	798	2	A28193	integrin beta-1* c
725	100	2.5	667	2	A48579	798	96	2.4	798	2	B28193	probable hormone r
726	100	2.5	873	1	A49729	799	96	2.4	886	2	A57172	LDL-receptor-relat
727	100	2.5	1122	2	I54237	800	96	2.4	4753	1	A47437	chymase (EC 3.4.21
728	100	2.5	1123	1	UN0712	801	95.5	2.4	177	2	S23505	probable regulator
729	100	2.5	1125	1	JH0771	802	95.5	2.4	218	2	H70770	probable serine pr
730	100	2.5	1151	2	I38004	803	95.5	2.4	330	2	B82415	ags protein precu
731	100	2.5	1156	2	I38005	804	95.5	2.4	427	2	JC4915	hypothetical prote
732	100	2.5	1251	2	A57293	805	95.5	2.4	561	2	T27318	mucin SMC (clone L
733	100	2.5	1299	2	T13251	806	95.5	2.4	1042	2	A57534	G2-G1 polypeptoin
734	99.5	2.5	330	2	I55975	807	95.5	2.4	1135	1	JQ1928	hypothetical prote
735	99.5	2.5	640	1	A30452	808	95.5	2.4	1270	2	T22615	peptidyl prollyl ci
736	99.5	2.5	686	2	S43562	809	95.5	2.4	3191	2	T39621	gastric mucin MUC5
737	99.5	2.5	914	1	S07047	810	95	2.4	463	2	T39621	LDL receptor prec
738	99.5	2.5	1280	2	A39117	811	95	2.4	850	2	S56015	hypothetical prote
739	99.5	2.5	1350	2	S00647	812	95	2.4	869	1	JC4858	mucin MUC5B, trach
740	99.5	2.5	1766	2	A42125	813	95	2.4	989	2	T01519	spermadhesin AQN-1
741	99.5	2.5	1847	2	T18308	814	95	2.4	1245	1	MMMSND	hypothetical prote
742	99.5	2.5	1984	2	T13171	815	95	2.4	1321	2	JEO352	LDL receptor precu
743	99	2.5	589	2	B38128	816	94.5	2.4	643	2	T25473	protein ZC84.1 (im
744	99	2.5	591	2	I48141	817	94.5	2.4	736	2	S47645	epidermal growth f
745	99	2.5	675	1	KQMS	818	94.5	2.4	862	1	QRMULD	insulin-like growt
746	99	2.5	675	1	KKRTS	819	94.5	2.4	862	1	QRMULD	platelet-derived g
747	99	2.5	805	2	S68441	820	94.5	2.4	1216	2	T26104	hypothetical prote
748	99	2.5	892	2	S68439	821	94.5	2.4	1416	2	E88550	neuregulin-3 (lmpo
749	99	2.5	894	2	S68437	822	94.5	2.4	1717	1	A45558	hypothetical prote
750	99	2.5	900	2	S68440	823	94	2.4	258	1	B37252	subtilisin-like pr
751	99	2.5	1162	2	S68438	824	94	2.4	370	2	JC7998	subtilisin-like pr
752	99	2.5	1558	2	A82457	825	94	2.4	634	2	T02594	PACB4 - mouse (fr
753	98.5	2.5	2809	2	I30213	826	94	2.4	736	2	T06757	paranodin - rat
754	98.5	2.5	317	2	T28605	827	94	2.4	899	2	G02428	neurexin IV - mous
755	98.5	2.5	317	2	F72172	828	94	2.4	915	2	JC6148	
756	98.5	2.5	317	2	G36855	829	94	2.4	932	2	I52527	
757	98.5	2.5	427	2	S74211	830	94	2.4	1381	2	T31083	
758	98.5	2.5	1178	1	A39804	831	94	2.4	1385	2	T14158	
759	98	2.5	82	2	T46510	832	94	2.4				

833	94	2.4	3097	2	T00021	DN-cadherin - fru1
834	93.5	2.4	256	2	A45403	insulin-like growth
835	93.5	2.4	317	2	T01789	BRK protein precu
836	93.5	2.4	449	2	TJ35048	probable ATP/GTP
837	93.5	2.4	456	2	T31483	hypothetical prote
838	93.5	2.4	466	2	S49820	PtII protein - Ara
839	93.5	2.4	612	2	TJ0799	laminin-related pr
840	93.5	2.4	739	2	B88553	protein K04H4.2b l
841	93.5	2.4	1115	2	S40241	G protein-coupled
842	93.5	2.4	1136	1	S57845	protein-tyrosine k
843	93	2.4	104	2	T19868	hypothetical prote
844	93	2.4	329	2	A48805	insulin-like growth
845	93	2.4	873	1	I48952	VDL receptor prec
846	93	2.4	995	2	A56599	embryo kinase 5 -
847	93	2.4	2767	1	U1HU	thyroglobulin prec
848	93	2.4	4545	1	S25111	alpha-2-macroglobu
849	92.5	2.3	211	2	A46458	human CRI homolog
850	92.5	2.3	736	2	T19366	hypothetical prote
851	92.5	2.3	756	2	S47656	hypothetical prote
852	92.5	2.3	803	1	IUCH3	TMDC II protein -
853	92.5	2.3	955	2	A45441	integrin, band 3 p
854	92.5	2.3	1367	1	IGHUR1	thrombospondin 4 -
855	92	2.3	334	2	T23027	insulin-like growth
856	92	2.3	650	2	A34498	hypothetical prote
857	92	2.3	719	2	T00266	glycoprotein anti
858	92	2.3	915	2	B48225	hypothetical prote
859	92	2.3	915	2	UC5545	probable proteoel
860	92	2.3	1097	2	S68685	integrin beta-4 pr
861	92	2.3	1444	2	T15856	angiogenesis inhib
862	92	2.3	1895	2	T15881	hypothetical prote
863	92	2.3	2533	2	T28675	alpha-5ID immobili
864	92	2.3	3869	2	A48205	All-1 protein +GTE
865	91.5	2.3	237	2	I47031	insulin-like growth
866	91.5	2.3	250	2	T30124	hypothetical prote
867	91.5	2.3	303	2	H35068	apolipoprotein H-r
868	91.5	2.3	511	2	T17298	hypothetical prote
869	91.5	2.3	588	2	T33815	hypothetical prote
870	91.5	2.3	640	2	S49932	MT30 protein - ye
871	91.5	2.3	1101	2	T16840	hypothetical prote
872	91.5	2.3	1161	2	D83076	type 4 fibrillar bi
873	91.5	2.3	2144	2	S71490	aah1 protein - fru
874	91.5	2.3	2672	2	A48126	translacton activa
875	91.5	2.3	2910	2	T42214	otogelin - mouse
876	91	2.3	94	2	PC2013	tissue kallikrein
877	91	2.3	293	2	T09065	hypothetical prote
878	91	2.3	319	1	I50370	transcription fac
879	91	2.3	398	2	E71539	hypothetical prote
880	91	2.3	435	2	I54182	tumor necrosis fac
881	91	2.3	478	2	S47040	gene Tf52 protein
882	91	2.3	909	1	ORXLU2	LDL receptor 2 pre
883	91	2.3	2543	2	T31687	surface antigen - p
884	91	2.3	4543	1	A53102	alpha-2-macroglobu
885	90.5	2.3	53	2	S17294	epidermal growth f
886	90.5	2.3	330	1	JN0561	urokinase-type pla
887	90.5	2.3	642	1	JP0079	LTM protein kinase
888	90.5	2.3	746	1	HYHUMA	megarin A (EC 3.4.2
889	90.5	2.3	776	2	S28258	androgen-regulated
890	90.5	2.3	960	2	JE0356	gamma-aminobutyric
891	90.5	2.3	1104	2	I38869	transcription fac
892	90.5	2.3	1148	2	GNVUNE	M polypeptide prec
893	90.5	2.3	1357	2	T16860	hypothetical prote
894	90.5	2.3	1436	2	A46496	antigen WC1.1 prec
895	90.5	2.3	2813	1	VWNU	von Willebrand fac
896	90	2.3	156	2	B23863	tissue kallikrein
897	90	2.3	340	2	T34423	hypothetical prote
898	90	2.3	409	2	T11743	hypothetical prote
899	90	2.3	417	2	T29864	hypothetical prote
900	90	2.3	522	2	T29767	integrin beta-6 ch
901	90	2.3	577	2	B37057	nicotinic denydroge
902	90	2.3	814	1	I39627	alpha-5ID-immobili
903	90	2.3	2533	2	T28674	DNA binding protei
904	89.5	2.3	417	2	T39939	endopeptidase 2 (E
905	89.5	2.3	748	2	S24134	
906	89.5	2.3	906	1	ORHYLD	LDL receptor precu
907	89.5	2.3	1164	2	T01871	RNA-directed DNA p
908	89.5	2.3	1258	2	A12155	WD-repeat protein
909	89.5	2.3	1664	2	T00250	MEGF2 protein - hu
910	89	2.3	319	2	A53502	folliclestin - Afri
911	89	2.3	354	2	T22274	hypothetical prote
912	89	2.3	369	2	F81178	histone deacetylase
913	89	2.3	390	2	C90208	hypothetical prote
914	89	2.3	469	1	NM1V27	exo-alpha-sialidas
915	89	2.3	525	2	T21357	hypothetical prote
916	89	2.3	907	2	I50404	p50B/p27 (Lyt-10)
917	89	2.3	1110	1	B42544	G2-G1 polypeptide
918	89	2.3	1170	2	A40558	thrombospondin 1 p
919	88.5	2.2	317	2	T37442	EBV gp42, ps/hr pro
920	88.5	2.2	356	2	T20656	hypothetical prote
921	88.5	2.2	438	2	T40509	lim domain protein
922	88.5	2.2	693	2	I37570	zinc finger protei
923	88.5	2.2	754	2	T47886	transketolase-like
924	88.5	2.2	905	2	S55059	feritin alpha-I -
925	88.5	2.2	1077	2	T41146	probable cysteine-
926	88.5	2.2	1096	2	T16875	hypothetical prote
927	88.5	2.2	1170	1	TSHUP1	thrombospondin 1 p
928	88.5	2.2	1978	2	T07081	acetyl-CoA carboxy
929	88	2.2	621	2	I38467	low density lipopr
930	88	2.2	656	2	UC2005	integrin beta-5 ch
931	88	2.2	798	2	B27079	fibronectin recept
932	88	2.2	799	2	A38308	integrin beta-5 ch
933	88	2.2	962	2	UC5571	subfollisin-like pr
934	88	2.2	1085	2	C96797	integrin-like pr
935	88	2.2	1175	2	S52417	unknown protein (I
936	88	2.2	1192	2	S69000	E-selectin ligand
937	87.5	2.2	554	2	A45818	laminin gamma 2 ch
938	87.5	2.2	580	2	A37107	cytolysin precursor
939	87.5	2.2	584	1	C8HUA	spermatogenesis pr
940	87.5	2.2	667	2	T01999	complement C8 alph
941	87.5	2.2	914	1	JC6150	hypothetical prote
942	87.5	2.2	1807	2	T16892	iodide peroxidase
943	87.5	2.2	1816	1	S68960	integrin beta-4 ch
944	87	2.2	387	2	I38449	extracellular prote
945	87	2.2	706	2	S74610	hypothetical prote
946	87	2.2	743	2	T40521	hypothetical prote
947	87	2.2	860	2	T16892	hypothetical prote
948	87	2.2	970	2	I78842	receptor protein-t
949	87	2.2	975	2	UC5570	subfollisin-like pr
950	87	2.2	1042	2	T26644	hypothetical prote
951	87	2.2	1056	2	A53767	hypothetical prote
952	87	2.2	1134	1	JN0711	mucin MUC5B, trach
953	87	2.2	1945	2	T13937	protein-tyrosine k
954	87	2.2	2481	2	A43908	plexin A - fruit f
955	87	2.2	3968	2	A44265	fibronectin - Afri
956	86.5	2.2	224	2	A44265	trichorax homolog
957	86.5	2.2	262	2	S72795	hypothetical prote
958	86.5	2.2	282	2	T16271	hypothetical prote
959	86.5	2.2	336	2	D69074	polyferredoxin 4x2
960	86.5	2.2	391	2	T34284	hypothetical prote
961	86.5	2.2	471	2	I79528	alkaline phosphata
962	86.5	2.2	585	2	I46686	complement compone
963	86.5	2.2	632	2	T21602	hypothetical prote
964	86.5	2.2	638	2	AF3463	flagellar protein
965	86.5	2.2	641	2	F71810	type III DNA modif
966	86.5	2.2	651	2	T05869	hypothetical prote
967	86.5	2.2	700	2	A32392	protein kinase C (
968	86.5	2.2	734	2	C81399	isochlorate denydro
969	86.5	2.2	1172	2	A42587	thrombospondin 2 p
970	86.5	2.2	1376	1	J01534	G2-glycoprotein pr
971	86.5	2.2	1478	2	D75281	ribonucleoside-dip
972	86.5	2.2	1473	2	A20872	ovostatin precursor
973	86.5	2.2	3712	1	YGCEVC	alpha-aminoadipyl-
974	86	2.2	455	2	B82525	conserved hypochet
975	86	2.2	713	2	A35502	major surface-labe
976	86	2.2	738	2	S40992	hypothetical prote
977	86	2.2	905	2	T23229	hypothetical prote
978	86	2.2	906	2	A71438	probable resistanc

979	86	2.2	933	1	OPHUT	iodide peroxidase	1052	83.5	2.1	311	2	JC7873	L-rihamose-binding
980	86	2.2	969	1	A39490	subtilisin-like pr	1053	83.5	2.1	344	2	A32141	foliistatin 1 prec
981	86	2.2	1487	1	S48719	phospholipase-A(2)	1054	83.5	2.1	348	2	T28623	hypothetical prote
982	86	2.2	1572	2	T00037	brain-specific ang	1055	83.5	2.1	354	2	G64475	GTP-binding protei
983	86	2.2	1650	2	S53457	dominant autoantig	1056	83.5	2.1	358	1	A55973	transcription fact
984	86	2.2	2233	2	T28659	surface protein 51	1057	83.5	2.1	366	2	I53035	trithorax homolog
985	85.5	2.2	317	2	A84933	ps/hr protein - va	1058	83.5	2.1	491	2	H83770	hypothetical prote
986	85.5	2.2	340	1	B55973	transcription fact	1059	83.5	2.1	579	2	B84192	pyruvate kinase [l
987	85.5	2.2	344	1	A27701	collagenin precur	1060	83.5	2.1	589	2	C38128	epithelin/granulin
988	85.5	2.2	358	2	B64427	carbamoyl-phosphat	1061	83.5	2.1	697	2	H86457	76 kD hypothetical
989	85.5	2.2	463	1	A36479	milk fat globule m	1062	83.5	2.1	873	2	D88482	protein C05D11.8 [
990	85.5	2.2	515	2	T05863	hypothetical prote	1063	83.5	2.1	1106	2	T13938	gene shuttles craft
991	85.5	2.2	638	2	S22491	acetylactate synth	1064	83.5	2.1	2120	2	T30243	alpha tectorin - c
992	85.5	2.2	663	2	T21010	hypothetical prote	1065	83.5	2.1	2704	2	S09118	G surface protein
993	85.5	2.2	798	2	S01659	integrin beta-1 ch	1066	83.5	2.1	4302	2	A38971	polysaccharide kidn
994	85.5	2.2	1162	2	PC4184	lactin receptor, O	1067	83.5	2.1	13055	2	T16580	hypothetical prote
995	85.5	2.2	1229	2	H84455	hypothetical prote	1068	83	2.1	304	2	A83513	probable transcrip
996	85.5	2.2	2452	1	RNZQ2L	DNA-directed RNA p	1069	83	2.1	351	2	S20078	NOV protein - chic
997	85.5	2.2	2457	2	T18492	hypothetical prote	1070	83	2.1	372	2	T39244	probable phospho-2
998	85	2.2	200	2	T42678	hypothetical prote	1071	83	2.1	451	2	F83747	denosylmethionine-
999	85	2.2	291	2	I38098	L-plasminogen acti	1072	83	2.1	492	2	D35114	anthranilate synth
1000	85	2.2	318	2	H86342	hypothetical prote	1073	83	2.1	593	1	GYHU	granulin precursor
1001	85	2.2	343	2	S55359	foliistatin - chic	1074	83	2.1	770	2	S04847	leukocyte adhesion
1002	85	2.2	359	1	I51734	transcription fact	1075	83	2.1	770	2	D89447	protein F57C12.1 [
1003	85	2.2	413	2	T23098	hypothetical prote	1076	83	2.1	771	2	A45839	leukocyte adhesion
1004	85	2.2	542	2	A84554	hypothetical prote	1077	83	2.1	800	2	S54623	probable mtochond
1005	85	2.2	552	2	F83417	sulfite reductase	1078	83	2.1	816	2	C69493	hypothetical prote
1006	85	2.2	606	2	S43118	finger protein - m	1079	83	2.1	1046	2	F71432	hypothetical prote
1007	85	2.2	638	2	S22490	acetylactate synth	1080	83	2.1	1066	2	B95037	hyaluronidase [lmp
1008	85	2.2	653	2	G96675	hypothetical prote	1081	83	2.1	1111	2	T00324	hypothetical prote
1009	85	2.2	671	1	UYPV19	noncapsid protein	1082	83	2.1	1373	2	JE0095	gastric mucin MUC5
1010	85	2.2	752	1	T26508	hypothetical prote	1083	83	2.1	2116	1	ZLVNSY	genome polyprotein
1011	85	2.2	794	2	F88508	protein H1412.6 [1084	83	2.1	3020	2	A43932	mucin 2 precursor,
1012	85	2.2	895	2	S74225	leptin receptor, i	1085	82.5	2.1	328	2	F83599	hypothetical prote
1013	85	2.2	1021	2	S26985	probable DNA-direc	1086	82.5	2.1	429	2	A42872	coagulation factor
1014	85	2.2	1078	2	F97907	hyaluronate lyase	1087	82.5	2.1	466	2	S29302	complement C8 beta
1015	85	2.2	1148	1	JQ1604	M polyprotein prec	1088	82.5	2.1	591	1	C8HUB	allilin lyase [EC 4
1016	85	2.2	1533	1	T00344	hypothetical prote	1089	82.5	2.1	753	2	T19338	hypothetical prote
1017	85	2.2	1538	2	S73296	glutamate synthase	1090	82.5	2.1	761	2	E82223	ribonucleoside-dip
1018	85	2.2	2150	2	T32497	hypothetical prote	1091	82.5	2.1	781	2	S43534	integrin beta3 - c
1019	84.5	2.1	271	2	S12783	OX40 antigen precu	1092	82.5	2.1	984	2	T00326	hypothetical prote
1020	84.5	2.1	337	2	I47079	foliistatin - shue	1093	82.5	2.1	1175	2	I57549	adenosine deaminas
1021	84.5	2.1	344	2	I45894	foliistatin - bov1	1094	82.5	2.1	1372	2	A34157	insulin receptor p
1022	84.5	2.1	429	2	T16556	hypothetical prote	1095	82	2.1	188	2	A39787	teratocarcinoma-de
1023	84.5	2.1	494	2	A99683	alkaline phosphata	1096	82	2.1	235	2	AE0114	deoxyribonuclease
1024	84.5	2.1	494	2	A46570	H+-transporting tw	1097	82	2.1	338	2	S65019	chitinase [EC 3.2.
1025	84.5	2.1	505	2	A46570	finger protein (cl	1098	82	2.1	343	2	S45321	foliistatin - mous
1026	84.5	2.1	615	2	S06546	hypothetical prote	1099	82	2.1	349	2	D72175	G2R protein - vari
1027	84.5	2.1	654	2	T30136	GGBF family prote	1100	82	2.1	432	2	D83904	cabon storage regu
1028	84.5	2.1	696	2	A12849	GGBF family prote	1101	82	2.1	528	2	B42560	4-chlorobenzoate-C
1029	84.5	2.1	696	2	G97626	hypothetical prote	1102	82	2.1	583	2	T34121	steroide/thyroid/re
1030	84.5	2.1	744	2	A43353	acetic acidoligase	1103	82	2.1	599	2	B82439	formate-tetrahydro
1031	84.5	2.1	746	2	F87243	isocitrate dehydro	1104	82	2.1	711	2	T27358	hypothetical prote
1032	84.5	2.1	760	2	A40195	meprin A (EC 3.4.2	1105	82	2.1	868	2	T02635	D2 protein homolo
1033	84.5	2.1	788	2	A46547	platelet glycoprot	1106	82	2.1	1530	2	I45944	neurexin I - alpha
1034	84.5	2.1	789	2	S28259	androgen-regulated	1107	82	2.1	1609	2	S44821	F4482.4 protein -
1035	84.5	2.1	864	2	T49574	probable carnitine	1108	82	2.1	1661	2	T13130	head-activator bin
1036	84.5	2.1	917	2	I48950	telencephalin prec	1109	82	2.1	2214	2	T16305	hypothetical prote
1037	84.5	2.1	950	2	T28793	diacylglycerol kin	1110	82	2.1	4861	2	S71752	giant protein p619
1038	84	2.1	278	2	T17178	hypothetical prote	1111	81.5	2.1	209	2	T02394	hypothetical prote
1039	84	2.1	335	2	T23657	hypothetical prote	1112	81.5	2.1	251	2	A55035	cysteine-rich prot
1040	84	2.1	349	2	D36858	gene G4R protein -	1113	81.5	2.1	349	2	S57453	polyferredoxin 4x2
1041	84	2.1	413	2	T34123	hypothetical prote	1114	81.5	2.1	383	2	D88633	protein P56B3.2 [l
1042	84	2.1	471	2	A84741	probable myrosinas	1115	81.5	2.1	429	2	S01919	knirps protein - f
1043	84	2.1	520	2	G88846	protein T124V.2 [l	1116	81.5	2.1	432	2	A25483	env polyprotein, r
1044	84	2.1	567	2	T49942	hypothetical prote	1117	81.5	2.1	443	2	T29147	hypothetical prote
1045	84	2.1	972	2	A30363	glicoprotein GP330	1118	81.5	2.1	460	2	S67174	lysine decarboxyla
1046	84	2.1	1034	2	JC5598	mucin - rat	1119	81.5	2.1	482	2	A83655	probable finger pr
1047	84	2.1	1047	2	T34946	probable isoleucyl	1120	81.5	2.1	496	2	T08674	transketolase (EC
1048	84	2.1	1599	2	T16210	scavenger receptor	1121	81.5	2.1	519	2	S54300	hemagglutinin - ca
1049	84	2.1	2153	2	T14893	C4b-binding protei	1122	81.5	2.1	604	2	HMNZCD	hematopoietic grow
1050	83.5	2.1	202	1	A44247	probable pepetidas	1123	81.5	2.1	625	2	S35317	proto-oncogene - m
1051	83.5	2.1	278	2	AH0282		1124	81.5	2.1	626	2	S37622	

1125	81.5	2.1	724	2	A48569	antigen Em100 - E1	1198	80	2.0	644	2	I84634	Tamm-Horsfall prot
1126	81.5	2.1	977	2	S49004	cytochrome kinase Mp	1199	80	2.0	656	1	S59631	endo-1,4-beta-xyla
1127	81.5	2.1	1187	2	T18355	hypothetical prote	1200	80	2.0	680	2	PN0510	integrin beta-3 ch
1128	81.5	2.1	1220	2	D88013	protein K1084.1 (1	1201	80	2.0	713	2	UC6012	glutamine-fructose
1129	81.5	2.1	1507	2	A40228	neurexin I-alpha p	1202	80	2.0	741	2	G84888	probable transket
1130	81	2.1	180	2	AE1010	conserved hypochet	1203	80	2.0	746	2	G84605	hypothetical prote
1131	81	2.1	266	2	C81906	hypothetical prote	1204	80	2.0	753	2	UC7386	retinovin - chicke
1132	81	2.1	348	2	A56247	natural killer cel	1205	80	2.0	817	2	T24063	hypothetical prote
1133	81	2.1	428	2	T04472	probable pothobol	1206	80	2.0	902	2	T01127	curly leaf protein
1134	81	2.1	441	2	I40455	penicillin binding	1207	80	2.0	1138	2	T36406	hypothetical prote
1135	81	2.1	501	2	UC7181	maternal transcrip	1208	80	2.0	1184	2	A96638	hypothetical prote
1136	81	2.1	554	2	A31300	perforin precursor	1209	80	2.0	1342	2	A36223	kinase-related tra
1137	81	2.1	560	2	S25092	jasmolate-induced	1210	80	2.0	1385	2	H88569	protein K03H1.5 (1
1138	81	2.1	732	2	T52588	wall-associated se	1211	80	2.0	1409	2	S41028	hypothetical prote
1139	81	2.1	735	2	G02937	feritin beta - cr	1212	80	2.0	2219	2	T27684	hypothetical prote
1140	81	2.1	755	2	I48101	ADAM 6 protein pre	1213	80	2.0	2229	2	T16199	hypothetical prote
1141	81	2.1	769	1	UC1121	leukocyte adhesion	1214	80	2.0	2643	2	T29149	hypothetical prote
1142	81	2.1	787	2	T49614	related to tol pro	1215	80	2.0	3140	2	S47508	genome polypeptin
1143	81	2.1	799	2	UC4126	integrin beta olig	1216	79.5	2.0	71	2	A59412	KGD-bearing platel
1144	81	2.1	821	1	A39667	brain-derived neur	1217	79.5	2.0	217	2	D90033	conserved hypochet
1145	81	2.1	1166	1	S06142	protein-tyrosine k	1218	79.5	2.0	254	2	I48599	insulin-like growt
1146	81	2.1	1344	2	H84537	hypothetical prote	1219	79.5	2.0	254	2	UC1464	insulin-like growt
1147	81	2.1	1365	2	T00833	RNA-directed DNA p	1220	79.5	2.0	317	2	D64167	transaldolase (EC
1148	81	2.1	1438	2	A48216	neurexin III-alpha	1221	79.5	2.0	318	2	S43317	chitinase (EC 3.2.
1149	81	2.1	1471	2	B48218	neurexin III-alpha	1222	79.5	2.0	324	2	S20981	chitinase (EC 3.2.
1150	81	2.1	1578	2	I48216	neurexin III-alpha	1223	79.5	2.0	356	2	A25818	chitinase (EC 3.2.
1151	81	2.1	1895	2	T06609	disease resistance	1224	79.5	2.0	397	2	S49300	chromodulin - B
1152	81	2.1	3898	2	S57437	genome polypeptin	1225	79.5	2.0	451	2	C86464	hypothetical prote
1153	80.5	2.0	371	2	B72461	hypothetical prote	1226	79.5	2.0	474	2	A57480	tubulointerstitial
1154	80.5	2.0	390	2	T27256	hypothetical prote	1227	79.5	2.0	614	2	T40652	hypothetical prote
1155	80.5	2.0	409	2	B87661	conserved hypochet	1228	79.5	2.0	661	2	C85758	hypothetical prote
1156	80.5	2.0	416	2	S49821	hemorrhagic protei	1229	79.5	2.0	661	2	B90861	hypothetical prote
1157	80.5	2.0	421	2	S49821	hemorrhagic protei	1230	79.5	2.0	694	2	S58083	transketolase (EC
1158	80.5	2.0	434	2	T26654	PR12 protein - Ara	1231	79.5	2.0	700	1	HYH0MB	transketolase (EC
1159	80.5	2.0	471	1	PAECA	hypothetical prote	1232	79.5	2.0	713	2	I65253	disintegrin-like t
1160	80.5	2.0	479	2	D86182	alkaline phosphata	1233	79.5	2.0	741	2	T09015	meprin A (EC 3.4.2
1161	80.5	2.0	502	2	T16716	protein F13W7.11 (1234	79.5	2.0	868	2	G84674	transketolase (EC
1162	80.5	2.0	509	2	T22238	hypothetical prote	1235	79.5	2.0	952	2	T28792	probable selenium-
1163	80.5	2.0	516	2	S53007	hypothetical prote	1236	79.5	2.0	1161	1	S31213	diacylglycerol kin
1164	80.5	2.0	535	2	T21028	citrate synthase -	1237	79.5	2.0	1178	2	S08405	nidogen precursor
1165	80.5	2.0	570	2	T46261	hypothetical prote	1238	79.5	2.0	1260	2	A86323	hypothetical prote
1166	80.5	2.0	604	2	T15796	hypothetical prote	1239	79.5	2.0	1360	2	S51364	protein F14D16.3 (
1167	80.5	2.0	627	2	T00603	hypothetical prote	1240	79.5	2.0	1402	2	T24664	sperm tail-specific
1168	80.5	2.0	656	2	B49423	hypothetical prote	1241	79.5	2.0	2261	2	T07084	hypothetical prote
1169	80.5	2.0	658	2	A86828	semaphorin I - fru	1242	79.5	2.0	2499	1	A30788	acetyl-CoA carboxy
1170	80.5	2.0	673	2	A49878	transketolase (EC	1243	79	2.0	188	2	S57894	mannose 6-phosphat
1171	80.5	2.0	704	2	A48040	coagulation factor	1244	79	2.0	171	2	A30362	laminin - Hydrx vu
1172	80.5	2.0	741	2	B81143	meprin A (EC 3.4.2	1245	79	2.0	192	1	B57143	teratocarcinoma-de
1173	80.5	2.0	742	2	I37225	isocitrate dehydro	1246	79	2.0	192	2	AC0763	chitosulfate-dithio
1174	80.5	2.0	773	2	I46059	leucocyte antigen	1247	79	2.0	206	2	D97285	chitosulfate reduct
1175	80.5	2.0	1055	2	T05663	beta-1 integrin su	1248	79	2.0	360	2	S32695	ribosomal protein
1176	80.5	2.0	1119	2	A88481	hypothetical prote	1249	79	2.0	364	2	T24153	Wnt-2 protein - Ca
1177	80.5	2.0	1245	1	VHWV82	protein C16A3.6 (1	1250	79	2.0	392	2	T33444	hypothetical prote
1178	80.5	2.0	1376	1	VGIM42	structural polypro	1251	79	2.0	393	2	A64036	hypothetical prote
1179	80.5	2.0	1382	1	INHUR	E2 glycoprotein pr	1252	79	2.0	415	2	D87020	hypothetical prote
1180	80.5	2.0	1526	2	T19473	insulin receptor p	1253	79	2.0	417	2	T08724	probable membrane
1181	80.5	2.0	1558	2	C89114	hypothetical prote	1254	79	2.0	587	2	C85044	hypothetical prote
1182	80.5	2.0	1611	2	G84493	probable retroelem	1255	79	2.0	602	2	B81420	hypothetical prote
1183	80.5	2.0	2167	2	T34395	hypothetical prote	1256	79	2.0	606	2	T22105	GTP-binding protei
1184	80.5	2.0	2262	2	T30890	calcium channel al	1257	79	2.0	630	2	T48369	hypothetical prote
1185	80	2.0	211	1	CYRTB3	beta-crystallin B3	1258	79	2.0	660	2	S71949	hypothetical prote
1186	80	2.0	243	2	T27036	hypothetical prote	1259	79	2.0	687	2	T16352	metalloproteinase
1187	80	2.0	284	2	T25938	hypothetical prote	1260	79	2.0	729	2	A45716	hypothetical prote
1188	80	2.0	290	2	T46470	hypothetical prote	1261	79	2.0	738	2	T41730	leukemia virus cel
1189	80	2.0	335	2	A39743	u-plasminogen acti	1262	79	2.0	753	2	B36268	platelet glycoprot
1190	80	2.0	395	2	S64299	probable membrane	1263	79	2.0	773	2	JEO387	exo-alpha-sialidas
1191	80	2.0	398	1	S24802	polyferredoxin 6x2	1264	79	2.0	788	2	A60798	platelet glycoprot
1192	80	2.0	437	2	S05478	properdin - mouse	1265	79	2.0	788	2	I77349	platelet glycoprot
1193	80	2.0	464	2	H82928	ATP synthase beta	1266	79	2.0	790	2	D81668	phenylalanine-tRNA
1194	80	2.0	500	2	A36388	RNA-directed RNA p	1267	79	2.0	826	2	A60385	monocyte surface a
1195	80	2.0	589	2	I38598	zinc finger protei	1268	79	2.0	871	2	T04867	hypothetical prote
1196	80	2.0	642	2	C89124	protein K07C11.9 (1269	79	2.0	952	2	T18900	disintegrin and me
1197	80	2.0	644	1	A40212	uromodulin precurs	1270	79	2.0	1023	2	T30257	IgG Fc binding pro

1271	79	2.0	1289	1	RMXR3	mRNA guanylyltrans	1344	78	2.0	4085	2	S28600	hypothetical prote
1272	79	2.0	1391	2	T20406	hypothetical prote	1345	77.5	2.0	46	2	UT0747	epiregulin - rat
1273	79	2.0	1513	2	AS4895	mycin 2, intestina	1346	77.5	2.0	162	2	S68401	epiregulin precurs
1274	79	2.0	1522	2	T00028	brain-specific ang	1347	77.5	2.0	244	2	AB2505	histidine kinase-1
1275	79	2.0	1642	2	T19130	hypothetical prote	1348	77.5	2.0	255	2	H96776	hypothetical prote
1276	79	2.0	1777	2	T00490	nonstructural prot	1349	77.5	2.0	255	2	UC5559	hypothetical prote
1277	79	2.0	1777	2	AC2088	serine/threonine k	1350	77.5	2.0	296	2	G81111	lectin-B - Vigna
1278	79	2.0	1166	2	S65873	apernadhesin PSP-I	1351	77.5	2.0	400	2	AS5647	conserved hypochet
1279	78.5	2.0	307	2	S18523	fructokinase (BC 2	1352	77.5	2.0	402	2	S02029	phyllipoid - fruit
1280	78.5	2.0	327	2	AS5356	urukinae-type pla	1353	77.5	2.0	407	2	C82428	phosphoribulokinas
1281	78.5	2.0	341	2	I61725	natural killer as8	1354	77.5	2.0	413	4	FOHUE2	glucose-1-phosphat
1282	78.5	2.0	344	2	I57658	foliistatin - rat	1355	77.5	2.0	457	2	B85749	retrovirus-related
1283	78.5	2.0	355	2	C70457	hypothetical prote	1356	77.5	2.0	457	2	G90869	ATP-dependent RNA
1284	78.5	2.0	363	1	C55973	transcription fact	1357	77.5	2.0	457	2	B64884	ATP-dependent RNA
1285	78.5	2.0	376	2	E70361	chaperone DnaJ - A	1358	77.5	2.0	469	2	T36362	probable DNA repai
1286	78.5	2.0	389	2	D75180	hypothetical prote	1359	77.5	2.0	488	2	T21701	hypothetical prote
1287	78.5	2.0	401	2	S65138	hypocaprotein anti	1360	77.5	2.0	546	2	B75175	probable amadae -
1288	78.5	2.0	436	2	S06884	viD2 protein - Ag	1361	77.5	2.0	548	2	S38864	Ig epsilon chain C
1289	78.5	2.0	474	2	B38634	tumor necrosis fac	1362	77.5	2.0	559	2	S38864	probable transposo
1290	78.5	2.0	495	2	AS7053	germ cell nuclear	1363	77.5	2.0	645	2	S20138	probable protein k
1291	78.5	2.0	507	2	T06452	probable legumin A	1364	77.5	2.0	717	2	B32838	DNA-directed RNA p
1292	78.5	2.0	517	1	FMWMA	legumin A precursor	1365	77.5	2.0	721	2	A39707	erythrocyte membra
1293	78.5	2.0	552	2	C45710	R transactivator h	1366	77.5	2.0	729	2	A69202	conserved hypochet
1294	78.5	2.0	600	2	I49281	fertilin alpha pre	1367	77.5	2.0	767	2	E85079	hypothetical prote
1295	78.5	2.0	638	2	D86477	protein F1504.27 l	1368	77.5	2.0	809	2	A57283	integrin beta chai
1296	78.5	2.0	658	2	F85024	probable GHP-rich	1369	77.5	2.0	845	2	G82773	phage-related prot
1297	78.5	2.0	662	2	I37892	IL12 receptor comp	1370	77.5	2.0	848	2	AF0020	nitrite reductase
1298	78.5	2.0	717	2	T25431	hypothetical prote	1371	77.5	2.0	933	2	A31930	cytoactin - chick
1299	78.5	2.0	748	2	T00732	hypothetical prote	1372	77.5	2.0	1017	2	D75028	h+-transporting AT
1300	78.5	2.0	757	2	T05688	hypothetical prote	1373	77.5	2.0	1079	1	TVFVMI	gag-RmlI-env poly
1301	78.5	2.0	763	2	I49089	hypothetical prote	1374	77.5	2.0	1142	2	A45031	cysteine-rich fibr
1302	78.5	2.0	842	2	T04555	hypothetical prote	1375	77.5	2.0	1333	2	E88257	protein let-23 lim
1303	78.5	2.0	1119	2	T16720	hypothetical prote	1376	77.5	2.0	1374	2	S70712	protein-tyrosine k
1304	78.5	2.0	1121	2	S57058	probable membrane	1377	77.5	2.0	2895	2	T08437	hyperplastic discs
1305	78.5	2.0	1131	2	T30951	hypothetical prote	1378	77.5	2.0	3085	2	T00327	polyprotein - infe
1306	78.5	2.0	1137	2	T18625	atrial natriuretic	1379	77	2.0	194	2	S70653	lectin heavy chain
1307	78.5	2.0	1188	2	UC4889	phosphatidylinosit	1380	77	2.0	230	2	T31722	hypothetical prote
1308	78.5	2.0	3473	1	A46112	genome polyprotein	1381	77	2.0	230	2	A44074	probable EGF-like
1309	78.5	2.0	3473	2	S27927	polyprotein - rice	1382	77	2.0	279	2	T16201	hypothetical prote
1310	78.5	2.0	3864	2	D87757	protein C4A4.1a l	1383	77	2.0	317	2	T45984	hypothetical prote
1311	78	2.0	247	2	T27778	hypothetical prote	1384	77	2.0	375	2	F70691	hypothetical prote
1312	78	2.0	334	2	T03157	probable capsid as	1385	77	2.0	452	2	H84772	probable serine ca
1313	78	2.0	360	2	T26037	hypothetical prote	1386	77	2.0	476	2	T19786	hypothetical prote
1314	78	2.0	360	2	G82994	glycine-cleavage s	1387	77	2.0	500	2	AE2032	glycerol kinase [i
1315	78	2.0	372	2	T31060	hypothetical prote	1388	77	2.0	502	2	T41148	trp-asp repeat con
1316	78	2.0	385	2	A81926	hypothetical prote	1389	77	2.0	535	2	T19706	hypothetical prote
1317	78	2.0	401	2	C89102	protein F2585.10 l	1390	77	2.0	540	1	OYHUCR	hypothetical prote
1318	78	2.0	404	2	T40553	trp-Aep repeat pro	1391	77	2.0	591	2	S33542	catechol oxidase (
1319	78	2.0	415	2	E83377	oxidoreductase Atu	1392	77	2.0	713	2	T40729	WD repeat-containi
1320	78	2.0	441	2	AH2930	probable alcohol d	1393	77	2.0	729	2	A49120	protein ZC123.1 [i
1321	78	2.0	446	2	P98351	tumor necrosis fac	1394	77	2.0	768	2	A87722	brain-derived neur
1322	78	2.0	454	1	GQMSRT	neurexin I-beta pr	1395	77	2.0	821	1	S06943	neuroal different
1323	78	2.0	468	2	B40228	T-cell glycoprotei	1396	77	2.0	1019	1	UC7538	hypothetical prote
1324	78	2.0	468	2	S26741	transmembrane gly	1397	77	2.0	1302	2	T00038	DNA segregation AT
1325	78	2.0	482	2	T17250	conserved hypochet	1398	77	2.0	1458	2	B97355	T2211.2 protein -
1326	78	2.0	522	2	A46103	importin alpha - c	1399	77	2.0	1733	2	G86344	receptor DRC-205 -
1327	78	2.0	523	2	C95303	prostaglandin-endo	1400	77	2.0	1743	2	S58880	hypothetical prote
1328	78	2.0	527	2	T04329	integrin beta-3 ch	1401	77	2.0	2165	2	T21371	hypothetical prote
1329	78	2.0	559	2	JH0259	hypothetical prote	1402	77	2.0	2165	2	T21371	hypothetical prote
1330	78	2.0	723	2	PN0509	epidermal growth f	1403	77	2.0	2584	2	T24158	hypothetical prote
1331	78	2.0	725	2	T27148	epidermal growth f	1404	77	2.0	2606	2	T24157	hypothetical prote
1332	78	2.0	843	2	A27131	hypothetical prote	1405	77	2.0	2769	2	UIBO	genome polyprotein
1333	78	2.0	957	2	T15976	hypothetical prote	1406	77	2.0	3033	1	GNWV78	dystrophin, muscle
1334	78	2.0	989	2	T47503	hypothetical prote	1407	77	2.0	3660	1	S02041	ALR protein - huma
1335	78	2.0	1016	2	G86295	hypothetical prote	1408	77	2.0	4957	2	T03455	platelet-aggregati
1336	78	2.0	1131	2	T38744	structural polypro	1409	77	2.0	5262	2	T03454	platelet-aggregati
1337	78	2.0	1245	1	VHMB	protein-tyrosine k	1410	76.5	1.9	71	2	AS9413	hypothetical prote
1338	78	2.0	1260	1	TVRTNU	epidermal growth f	1411	76.5	1.9	146	2	G95995	platelet aggregati
1339	78	2.0	1330	1	GOFFE	epidermal growth f	1412	76.5	1.9	216	2	TX0265	phosphoribosylform
1340	78	2.0	1339	2	JC4387	protein-tyrosine k	1413	76.5	1.9	224	2	AD2115	insulin-like growt
1341	78	2.0	1369	2	S70713	hypothetical prote	1414	76.5	1.9	254	2	T22380	hypothetical prote
1342	78	2.0	1658	2	D75489	Ran-binding protei	1415	76.5	1.9	264	2		
1343	78	2.0	3224	1	S58884		1416	76.5	1.9	272	2	AG2659	enoyl-(acyl-carrie

1417	76.5	1.9	272	2	E97451	hypothetical prote
1418	76.5	1.9	279	2	JC6565	four-and-a-half LI
1419	76.5	1.9	302	2	E86267	hypothetical prote
1420	76.5	1.9	322	1	S37344	chitinase (EC 3.2.
1421	76.5	1.9	333	2	T24836	hypothetical prote
1422	76.5	1.9	337	2	AC0156	probable cobalam
1423	76.5	1.9	359	2	T36050	probable histidin
1424	76.5	1.9	359	2	E83262	hypothetical prote
1425	76.5	1.9	385	2	AH0793	probable lipopolys
1426	76.5	1.9	386	2	TI1257	hypothetical prote
1427	76.5	1.9	388	2	EHMS	Ig epsilon chain C
1428	76.5	1.9	420	2	S74388	gamma-glutamyl pho
1429	76.5	1.9	435	2	T25350	hypothetical prote
1430	76.5	1.9	481	2	A56346	transcription fact
1431	76.5	1.9	483	2	T48328	importin alpha-lik
1432	76.5	1.9	487	2	T21384	hypothetical prote
1433	76.5	1.9	504	2	T33404	hypothetical prote
1434	76.5	1.9	518	2	G88961	protein P59A7.8 [1
1435	76.5	1.9	520	2	C70311	hypothetical prote
1436	76.5	1.9	536	1	A39036	H+-transporting tw
1437	76.5	1.9	545	1	PMBXA	hypothetical prote
1438	76.5	1.9	601	2	T34396	hypothetical prote
1439	76.5	1.9	623	2	S56206	probable membrane
1440	76.5	1.9	658	2	T47960	hypothetical prote
1441	76.5	1.9	707	2	S68858	finger protein - m
1442	76.5	1.9	712	2	TI6338	hypothetical prote
1443	76.5	1.9	722	2	S32659	integrin beta 2 ch
1444	76.5	1.9	837	2	A42112	musclin-like peptid
1445	76.5	1.9	849	2	I50617	starch phosphoryla
1446	76.5	1.9	1000	2	S47243	hypothetical prote
1447	76.5	1.9	1004	2	T31665	suppressor protein
1448	76.5	1.9	1056	2	TI33167	hypothetical prote
1449	76.5	1.9	1071	2	TI8307	DNA polymerase III
1450	76.5	1.9	1153	2	T00615	RNA polymerase (be
1451	76.5	1.9	1201	2	AD1107	aldehyde-CoA carbox
1452	76.5	1.9	1349	2	T01699	vitellinogen vit-6
1453	76.5	1.9	1561	2	S46200	acetyl-CoA carboxy
1454	76.5	1.9	1660	2	TI8561	hypothetical prote
1455	76.5	1.9	1738	2	C84507	Munc13-2 - rat
1456	76.5	1.9	1985	2	I61776	protein CTRP - mal
1457	76.5	1.9	2098	2	TI18397	alpha tectorin - m
1458	76.5	1.9	2155	2	T30197	surface protein ty
1459	76.5	1.9	2395	1	S50820	xin protein - chic
1460	76.5	1.9	2562	2	TI4266	trichoxin protein
1461	76.5	1.9	3828	2	TI1857	hypothetical prote
1462	76.5	1.9	4550	2	TI18440	herc2 protein - mo
1463	76.5	1.9	4836	2	TI14346	tissue kallikrein
1464	76.5	1.9	96	2	A05308	sperm motility inh
1465	76.5	1.9	136	2	S72508	teratocarcinoma-de
1466	76.5	1.9	171	2	I49612	hypothetical prote
1467	76.5	1.9	233	2	T22396	rRNA methylase, YS
1468	76.5	1.9	261	2	G97190	paired box transcr
1469	76.5	1.9	269	2	S36166	conserved hypochet
1470	76.5	1.9	287	2	A11072	hypothetical prote
1471	76.5	1.9	333	2	TI5257	transcription fact
1472	76.5	1.9	349	1	I51739	membrane-associate
1473	76.5	1.9	374	2	A42264	hypothetical prote
1474	76.5	1.9	415	2	T32467	hypothetical prote
1475	76.5	1.9	418	2	T24350	oxidoreductase - D
1476	76.5	1.9	454	2	D75446	probable ADA-like
1477	76.5	1.9	490	2	T35948	purh bifunctional
1478	76.5	1.9	512	1	DTBSPH	hypothetical prote
1479	76.5	1.9	531	2	T22021	2-aminobenzoyl-Co
1480	76.5	1.9	603	2	S22402	metallopeptidase
1481	76.5	1.9	612	2	S71630	WD-repeat protein
1482	76.5	1.9	625	2	T39666	probable RNA-dirac
1483	76.5	1.9	626	1	RRVOWA	hypothetical prote
1484	76.5	1.9	634	2	AG0252	probable DEAD box
1485	76.5	1.9	634	2	AG0252	transketolase (imp
1486	76.5	1.9	637	2	A12223	furin (EC 3.4.21.7
1487	76.5	1.9	837	2	S43656	EBD kinase activa
1488	76.5	1.9	860	2	JC5702	hypothetical prote
1489	76.5	1.9	897	2	S67283	

1490	76	1.9	908	2	T27117	hypothetical prote
1491	76	1.9	925	2	T37475	lipoprotein recept
1492	76	1.9	926	1	OPPGIT	iodide peroxidase
1493	76	1.9	934	1	A34372	complement C6 prec
1494	76	1.9	967	2	T48210	hypothetical prote
1495	76	1.9	1001	2	AG1979	hypothetical prote
1496	76	1.9	1084	2	TI8292	nicotinamide nucle
1497	76	1.9	1097	2	SI7308	leukemia inhibitor
1498	76	1.9	1206	2	TI8557	probable hydrogena
1499	76	1.9	1245	1	VHWB2	structural polypro
1500	76	1.9	1385	2	S34230	156k protein - Pla

ALIGNMENTS

RESULT 1

hypothetical protein DKFZp586H2123.1 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C/Accession: T08805

R/Annotator: W. J. Wilkner, U. J. Mewes, R. W. J. Gassenhuber, J. J. Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A/Reference number: Z16472

A/Accession: T08805

A/Molecule type: mRNA

A/Residues: 1-181 <ANS>

A/Cross-references: UNIPROT:Q9Y432; UNIPARC:UPI000070151; EMBL:AL050214

A/Experimental source: adult uterus; clone DKFZp586H2123

C/Genetic: A/Note: DKFZp586H2123.1

Query Match Best Local Similarity 24.1%; Score 949; DB 2; Length 181; Pred. No. 6; 8e-57;

Matches 180; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	540	SLQISAIILHPNYPDILLDDADILKLDKARISTRVQPICLAASRLSTSPQESHITVA	599
DB	1	SLRISAIILHPNYPDILLDDADILKLDKARISTRVQPICLAASRLSTSPQESHITVA	60
QY	600	GMNVLDVSPGPKNDTLRSQGVSVVDSILCEQHEHDGIPVSTNMFCASWEPTAPSD	659
DB	61	GMNVLDVSPGPKNDTLRSQGVSVVDSILCEQHEHDGIPVSTNMFCASWEPTAPSD	120
QY	660	ICTAETGCIAAVSFPGRASPEPRMHLGIVSYDTCSHRLSTAFKYLFPKDWIERNM	719
DB	121	ICTAETGCIAAVSFPGRASPEPRMHLGIVSYDTCSHRLSTAFKYLFPKDWIERNM	180
QY	720	K 720	
DB	181	K 181	

RESULT 2

A38738 coagulation factor C precursor - horseshoe crab (Trachyleus tridentatus)

N/Content: names: coagulation-complement factor C; Limulus factor C

C/Species: Trachyleus tridentatus

C/Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004

C/Accession: A38738; B38738; S00105

R/Muta, T. J. Miyata, T. J. Matsuura, Y. J. Tokunaga, F. J. Nakamura, T. J. Toh, Y. J. Ikehara, Y. J. I

A/Title: Limulus factor C. An endotoxin-sensitive serine protease zymogen with a mosaic

A/Reference number: A38738; PMID:91177916; PMID:2007602

A/Accession: A38738

A/Molecule type: mRNA

A/Residues: 1-1019 <MUT>

A/Cross-references: UNIPROT:P28175; UNIPARC:UPI000012E5D2; GB:D90271; NID:g217396; PID:

A/Accession: B38738

A/Molecule type: mRNA

A/Residues: 1-466, 616, 'DN', 619-620, 'A', 622 <MUT>

125 C-MRGQVLRAPKGGIILT-----ESYPNANACEITTHAKPGFVQLRFLVMSLEDPV-- 176
 Db CRVESDNLFTQRCGVITSPDPENPYKSSSECLYITLIEBGFVWLOPEDT---FDIODH 237
 177 ---CQDYVEVRDGDNDGQIIRKVCNENRPAPIQISGSLHVLVFNHSDGKNDFPHAI 232
 Db PEVPCPYDIKIKVGP-----KVLGPFCEKAPFISTQSHSVLLTFHSDNNAENRWML- 292
 223 YBEITACSSSCFHDGTCVLDKAGYKACACLAGTGORCEVLEBRKNSCDGGPVNYQK 292
 Db -----SYRAA-----GNCCPEL-----QP--PVH----- 309
 293 ITGGPGLINGHAKIGTVVSFF-----CNNSY-VLSGNEKR-----TCQONEMSGQ 339
 Db -----GKIEPQAKT-----FFKQGVVSCDTGVYKLDONVEMDTFQIECLDKDGWSKI 359
 310 -----GKIEPQAKT-----FFKQGVVSCDTGVYKLDONVEMDTFQIECLDKDGWSKI 359
 340 PIC-IKACREPKISDLVRRVRLPMQVQRETPPLHOLYSAAFSKOKLQSAPTKKPALPFGD 398
 Db PTCKLVDCRAP-----GE 372
 360 PTCKLVDCRAP-----GE 372
 399 LPMGYQHLHT-----QLOYECISPPYRLGSSR--RTCLRTGKS---GRA-PSC 442
 Db -----LEHGITESTRNLTLYKSEIKYSCQEPYKMLNNTGTYCSAQGVMMNKVYLSRPTC 432
 373 LEHGITESTRNLTLYKSEIKYSCQEPYKMLNNTGTYCSAQGVMMNKVYLSRPTC 432
 443 IPIG-----KINITAPKQGLRMPQOALYRTSGVHDSGLHKAMFLVCSGA 492
 Db LPVCLPKPRSRKLMARIFN-GRPAQKGT-PIAIAL-----SHLNQPF--CGGS 478
 493 LVNERTVVAACHV---TDLGKVT-----MIKTADLVKLVGKFYDDDRDEKTIQSLDIS 544
 Db LIGSSWITTAACHQSLDPPDPTLRBDDLSPSPFKIILGKHW--LRSENEOHLGVK 536
 479 LIGSSWITTAACHQSLDPPDPTLRBDDLSPSPFKIILGKHW--LRSENEOHLGVK 536
 545 ALIHPNYDPIILDADIALKLKLDKARISTRVQPICLAASBDLSTFQGE-SHITVAGNV 603
 Db HTTHLPQDPTMFENDVALVELLESPLVNAFVMPICLEPGQ-----QEGAMVIVSGMK 591
 537 HTTHLPQDPTMFENDVALVELLESPLVNAFVMPICLEPGQ-----QEGAMVIVSGMK 591
 604 LADVSPKPKNDTLRSVSVVDSLLCEQHEHDHPIPVSYVDNMFCSAWETPAASDICTA 663
 Db QFLOFPP---ETLMEIRIPYDHSCTCKAYAP--LKKRVTRDMICAG-EKEGGKDACG 644
 592 QFLOFPP---ETLMEIRIPYDHSCTCKAYAP--LKKRVTRDMICAG-EKEGGKDACG 644
 664 ETGGAIAVSPFORASPEPRMHLMLGLVSWSYDKTCSHRLSTAFKVLPEKMIER 717
 Db DSGGMVTLNBERG---QWYLVGVSWGDDCGKDKRYG-VYSYIHNNKMWIOR 693

RESULT 4
 CIPHER
 Complement subcomponent C1r (EC 3.4.21.41) precursor [validated] - human
 C:Species: Homo sapiens (man)
 C:Date: 15-Nov-1984 #sequence revision 30-Jun-1991 #text change 09-Jul-2004
 C:Accession: A24170; A29768; A29769; S02422; A00916; A37820; S68830
 R:LeuTus, S.P.; Kuchali, K.; Sakarlassen, K.S.; Davie, E.W.
 Biochemistry 25, 4855-4863, 1986
 A>Title: Nucleotide sequence of the cDNA coding for human complement C1r.
 A:Reference number: A24170; MUID:87026566; PMID:3021205
 A:Accession: A24170
 A:Molecule type: mRNA
 A:Residues: 1-705 <LE>
 R:Journier, A.; Tosi, M.
 Biochem. J. 240, 783-787, 1986
 A>Title: Cloning and sequencing of full-length cDNA encoding the precursor of human comp
 A:Reference number: A29768; MUID:87156625; PMID:3030286
 A:Accession: A29768
 A:Molecule type: mRNA
 A:Residues: 1-151, 'L', 153-705 <D>
 R:Arlaud, G.J.; Willib, A.C.; Gagnon, J.
 Biochem. J. 241, 711-720, 1987
 A>Title: Complete amino acid sequence of the A chain of human complement-clasical-pathw
 A:Reference number: A29769; MUID:87241248; PMID:3036070
 A:Accession: A29769
 A:Molecule type: protein

A:Residues: 18-166, 'X', 168-463 <AR>
 A:Cross-references: UNIPARC:UPI0000172BC5
 A:Note: 152-Leu was also found
 R:Arlaud, G.J.; van Dorsselaer, A.; Bell, A.; Mancini, M.; Aude, C.; Gagnon, J.
 FEBS Lett. 222, 129-134, 1987
 A>Title: Identification of erythro-beta-hydroxyasparagine in the EGF-like domain of hum
 A:Reference number: S02422; MUID:88005128; PMID:2820791
 A:Accession: S02422
 A:Molecule type: protein
 A:Residues: 152-166 <AR>
 A:Cross-references: UNIPARC:UPI0000172BC6
 A:Note: 152-Leu was also found
 R:Arlaud, G.J.; Gagnon, J.
 Biochemistry 22, 1758-1764, 1983
 A>Title: Complete amino acid sequence of the catalytic chain of human complement subcomp
 A:Reference number: A00916; MUID:83204782; PMID:6303394
 A:Accession: A00916
 A:Molecule type: protein
 A:Residues: 464-705 <AR>
 A:Cross-references: UNIPARC:UPI000015033B
 R:Thieleens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.
 J. Biol. Chem. 265, 14469-14475, 1990
 A>Title: Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated NH
 A:Reference number: A37820; MUID:90354439; PMID:2387866
 A:Accession: A37820
 A:Molecule type: protein
 A:Residues: 18-26, 'L', 153-160, 'X', 252-255 <TH>
 A:Cross-references: UNIPARC:UPI0000172BC7; UNIPARC:UPI0000172BC8; UNIPARC:UPI0000172BC9
 R:Bellocq, S.; Thieleens, N.M.; Hudry-Clergeon, G.; Pelliot, Y.; Filhol, O.; Arlaud, G.
 FEBS Lett. 386, 15-20, 1996
 A>Title: Identification of a cryptic protein kinase CK2 phosphorylation site in human c
 A:Reference number: S68830; MUID:96221263; PMID:8635594
 A:Accession: S68830
 A:Molecule type: protein
 A:Residues: 133-137, 187-211, 610-613 <PR>
 A:Cross-references: UNIPARC:UPI0000172BCA; UNIPARC:UPI0000172BCB; UNIPARC:UPI0000172BCC
 A:Experimental source: Plasma
 C:Comment: C1r is a dimer of identical chains, each of which is activated by cleavage in
 A chain, while fragment gamma remains disulfide-bonded to the B chain to form C1r II.
 C:Comment: This protein is a serine protease that combines with C1q and C1s to form C1,
 n, activate C2 and C4.
 C:Genetics:
 A:Gene: GDB: C1R
 A:Cross-references: GDB:119729; OMIM:216950
 A:Map position: 12p13-12p13
 C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
 C:Keywords: acute phase; beta-hydroxyasparagine; calcium binding; complement pathway; d
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:17-138/Domain: C1r/C1s repeat homology <C1R1>
 F:18-463/Product: complement C1r chain A #status experimental <ACH>
 F:146-189/Domain: EGF homology <EGF>
 F:133-302/Domain: C1r/C1s repeat homology <C1R>
 F:297-463/Product: C1r gamma fragment #status experimental <GFR>
 F:309-371/Domain: complement factor H repeat homology <FHL>
 F:376-447/Domain: complement factor H repeat homology <FHL2>
 F:464-705/Product: complement C1r chain B #status experimental <BCH>
 F:464-697/Domain: trypsin homology <TRY>
 F:71-89, 146-165, 161-174, 176-189, 193-220, 250-268, 309-358, 338-371, 376-429, 406-447, 451-577,
 F:128, 221, 514, 581/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:167/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
 F:206/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status experiment
 F:463-464/Cleavage site: Arg-Ile (autolytic) #status experimental
 F:502, 557, 654/Active site: His, Asp, Ser #status predicted

Query Match 10.2%; Score 403.5; DB 1; Length 705;
 Best Local Similarity 22.9%; Pred. No. 1,6e-19;
 Db 69 EGGCYDDVAKTSADKSGIFGCGQLGSPPLGNPPEKKEFMGSGNKMILLTFHTDFSENEN--G 126
 Matches 178; Conservative 96; Mismatches 259; Indels 245; Gaps 41;
 44 ECGEYDIEC-----VC-----PKREYVGTITPC-----RNEENEC 77
 78 SCLHPCITF---ENCKSGRNGSWGTTLD-----DPYKGFYCAECRAGM----- 120

Dd 127 TIMEFYGFLAYVQAVDDECASSRSKSGEEDPQCQHLCNHYVGGFYGS-CRPGYELOED 185
Oy 121 ---YGGDCMRGGOVLRAPKQOI-LLE---SYPLNAHCEWTIHAKPGFYLQLRPFVMSLSEF 173
Db 186 RHSCQAEC--SSELTYASAGYSISLEYPRSYPPDLRCNVYSIRVERGLTLHLKFLB---PF 240
Oy 174 D-----YMGQYVVEVRDDDNRDQIHKRCNGNERAPAIQSITGSLHYLFHSDSGRAND 227
Db 241 DIDDHQOVHPYQLQI----YANGKNIGFCGKRPPDLLTSSNAVDLLFTFDSDGSR 296
Oy 228 GFHAIV-EELITACSSSPCFHDGTCLVLDKAGSYKCACLGYTGQRCENLLEBRNCSDPGSP 286
Db 297 GWKLRTTELIIKKRPPKLTDBFTTIQMLPOYO---FPDYFIATCK----- 339
Oy 287 VNGYQKITGGPGGLINGHAKIGTVVSFFCNNSYVLGNENKTRCOQNGEMSGKOPIC-1KA 345
Db 340 -CGYQLIEGNQVL-----HSFT-----ANCQDDGTTHRAMPRKIXD 375
Oy 346 CHEPKISDLVRRKRVLPWQVSRETPHLQLYSAAFSKOKLSAPTYKKPALPDGL---PM 401
Db 376 CGQPR-----MLPNGDFRYTMTM 393
Oy 402 GYQHLHTOLOEGCISPYFR---RLGSSNR-----TCLRTKGMSG-----RAPSCIPIGCK 448
Db 394 GNVTYARLIQYCHEPYYKMOTRAGSRESEGCVTTCTAGIKWKNEKGEXILPCRLPVCSK 453
Oy 449 IEN-----ITAPKTQGLRWPMQAAIYRRTSGVHDSGLHGAMFLVCSCALVNERTVV 500
Db 454 PVNPVQRORRIIGQKXKMGNFPMQV-----FTNIHG-----RG-----CGALLDGWRWL 498
Oy 501 VAACHCTDLGKTMIKTAADLKVYLGFKYRDDDRDKETIQSLQ-----ISAIIHPNY-- 552
Db 499 TAAHTLYLPKEHEAO-SNASLDVFLG-----HTNVEELMKLGNNHPIRRYSVHPDYHQ 548
Oy 553 -DPILLDAIDIAIKLBDKARISTRVOPICLAARDLSTSPQSHI-TVAGMWLVLD----- 606
Db 549 DESYNREGDIALLENSVTLGPVLLPICLP---DNDTFYDIGLMGVYSGFGVMEEKIN 605
Oy 607 ---VASPGFKNDTLRSGVSVSDSLCEQEHEDHGIPVSYTDNMFCASWEPTAPSICT 662
Db 606 DLRFVLP-----VANPQACENMLRGKRMADVFSQNNFCAG-HPSLKDQAO 651
Oy 663 AETGGIAANVPGRASPEPRMMLGLVSWSTDKTSCHSLSTAIFYLPPKMDIERNMK 720
Db 652 GDSGVFAVARDPN---TDRWVATGIVSWGIG-CS-RGYGFTYVLNVYDWIKKEME 702

RESULT 5
A59271
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
N|Alternate names: mannoside binding protein-associated serine proteinase 2 (MASP-2)
C|Species: Homo sapiens (man)
C|Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
Accession: A59271
R|Title: S.; Vorup-Jensen, T.; Stover, C.M.; Schwaebler, W.J.; Laursen, S.B.; Poulsen, K.
Nature 366, 506-510, 1997
A|File: A second serine protease associated with mannan-binding lectin that activates
Reference number: A59271; MUID:97242412; PMID:9087411
Accession: A59271
Status: nucleic acid sequence not shown; not compared with conceptual translation
Molecule type: mRNA
Residues: 1-686 <JEN>
Cross-references: UNIPROT:O00187; UNIPARC:UPI0000047562; GB:Y09926; NID:g4007626; PION
Experimental source: tissue liver
Note: submitted to GenBank, December 1996
Note: parts of this sequence, including the amino end of the mature protein, were deter
Gene: GDB:MASP2
Cross-references: GDB:6071500
Map position: lp36.2-lp36.3
Superfamily: complement-activating serine proteases Clr/Cls/MASP; Clr/Cls repeat homol
Keywords: beta-hydroxyaspartagine; complement pathway; duplication; hydrolase; serine p

F.1-15/Domains:signal sequence #stratus predicted <SIG>
F.15-444.445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F.19-134/Domains: C1r/C1s repeat homology <C1R1>
F.142-180/Domains: BGF homology <BGF>
F.184-293/Domains: C1r/C1s repeat homology <C1R2>
F.300-361/Domains: complement factor H repeat homology <FH1>
F.366-430/Domains: complement factor H repeat homology <FH2>
F.445-679/Domains: trypsin homology <TRY>
F.172-90.142-156.152-165.167-180.184-211.241-259.300-348.328-361.366-412.396-430.424-552
F.158/Modified site: erythro-beta-hydroxycarboxamide (asn) #status predicted
F.444-445/Cleavage site: Arg-Ile (autolytic) #status predicted
F.483.532.633/Active site: His, Asp, Ser #status predicted

Query Match	10.2#:	Score	400	5:	DB	1:	Length	666:
Best Local Similarity	22.7#:	Pred.	No.	2.5e-19:				
Matches	173:	Conservative	78:	Mismatch	245:	Indels	267:	Gaps
QY	128	CGOYLR--APK-----	GQILLESYP-----	LNACCEWTHAKPGFVIQLRVMLSLEDY	175			
Db	11	CGSATVPLGPFMPPEVFCGRILASPPGFGVANDQGRNRWTLTAPPGYRLRLRYTHTHDLELSH	70					
QY	176	MCQYDYVEVRDGDNRDGOIKRVCGNE---	RPPD---	IDSIGSLHVLPHSDGS--KN	225			
Db	71	LCEVDPVVLSSG----	AKVLATLTCGSESTDERAPGKDTFPYSLSSLSDITFRSDYSNEKP	126				
QY	226	FDGFHAIR--SEITACSSSP-----	CFPDGTCVLDKAGSYKACIAGYTGQR-----	CENTL	274			
Db	127	FTGPEAFYAADIDECQVAPGEAATCTDHH--	CHNHLDGFPYCSCRAGYVHLHRNKRTGAL	183				
QY	275	-----	LEE-----	277				
Db	184	CSGVFTQSGELSSPEYRPYPPLSSCTYSISLEGFSVILDFVESPDVETHPETLCY	243					
QY	278	-----	RNCSDP	283				
Db	244	DLFKIQDREHHPGCGKTLPHRIETYSNTVTTITFVDESGDHTGWKIHYTSTAHCYP	303					
QY	284	GAPVNGYOKITGGFGLINGRHAK--IGTVASFPCNNSY--VLSG----	NEKRTCOQNGEW	335				
Db	304	MAPRNGH-----	VSPQAKXILNDSFISIFETGELLGHLPLKSFYAVQXQKDSW	354				
QY	336	SGKQPI-C-IAKCREPKISDLVRNRYLPMQVOSRETPHLQYLSAAPSOKLOSAPTKPAL	394					
Db	355	DRPMACISIVCGPP--DDLPSGRV-----	EYITGP-----	383				
QY	395	PFQGLPMQYQHLHQLOYECISPPRY--RRLSSRRRTCLRTGKWSG--	RAPSCPICGK	448				
Db	384	-----	GVTTYKAVLIQYSCETETTYMKVNDGKYVCADGFWTSSKGEKSLPVECPVGL	436				
QY	449	IENITAPKTOGLR-----	WPMQAIYKRTSGVDGSLHKQAMFLVCSGALVNERTVVA	502				
Db	437	SARTTGGIYGGQAKRPDPFMQVLLIGTT--	AAGALLYDNWVLTJA	481				
QY	503	AHCTYDLGKVTMITADLKVVLGKFRYRDDREKTIQSLQ-----	ISAILHPNY--DP	554				
Db	482	AHAAYE-----	OKHDASALDIRMG-----	TLKLISHYTOAMSEAVFIHEGYTHD	526			
QY	555	ILLADADIALLLDKARISTRVOPICLAASRDLSFQESHITVAGMWVLADVSPGKN	614					
Db	557	AGFDDIDLILIKANNVIVINSITPPLCIPKKAESPMRTDIDIGTSGWC----	LTOGRLA	582				
QY	615	DTLRSGVSVVDSLICEOHEDHGIP--VSVDNNFFCASWEPTASDICTAETGIAAASF	673					
Db	583	RNLMYVDPIYDHQKCTAAAYEKPPYPRESVTANMLCAGLE--SGGDSGRDGGSG--	ALVVF	639				
QY	674	PGRASPEPRHMLGVSWSYDKTCSHRLSTAFYKVLPPKQMI	716					
Db	640	--LDSETERWFEVGGIVSGWSNMCEBAGQYGVYIVIVINPIE	680					

RESULT 6
S05008
complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - golden hamster

C:Species: Mesocricetus auratus (golden hamster)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S05008
R/Kinship: H.; Sakiyama, H.; Tokunaga, K.; Imajoh-Ohmi, S.; Hamada, Y.; Isono, K.; Sak
FEB8 Lett. 250, 411-415, 1989
A>Title: Complete primary structure of a calcium-dependent serine proteinase capable of
A/Reference number: S05008; PMID:89355606; PMID:2753140
A/Accession: S05008
A/Molecule type: mRNA
A/Residues: 1-695 <KIN>
A/Cross-references: UNIPROT:P15156; UNIPARC:UPI000012700B; EMBL:X16160; NID:G949621; PIRN
A/Note: part of this sequence, including the amino ends of both the heavy and light chain
C:Superfamily: complement-activating serine proteinases Clr/Cls/MASP: Clr/Cls repeat homol
C/Keywords: beta-hydroxyasparagine; calcium binding; duplication; glycoprotein; hydrolas
F1-21/Domain: signal sequence #status predicted <SIG>
F1-17-133/Domain: Clr/Cls repeat homology <CLR1>
F1-22-444/Product: serine proteinase heavy chain #status experimental <HCH>
F1-141-177/Domain: EGF homology <EGF>
F1-181-293/Domain: Clr/Cls repeat homology <CLR2>
F1-300-360/Domain: complement factor H repeat homology <FH1>
F1-365-428/Domain: complement factor H repeat homology <FH2>
F1-445-682/Domain: trypsin homology <TRY>
F1-446-695/Product: serine proteinase light chain #status experimental <LCH>
F1-71-89,141-153,149-162,164-177,181-208,240-257,300-347,327-360,365-410,392-428,432-556,
F1-55/Modified site: erythro-beta-hydroxyasparagine (asn) #status predicted
F1-180,413/Binding site: carbohydrate (asn) (covalent) #status predicted
F1-482,536,638/Active site: His, Asp, Ser #status predicted

Query Match 9.6%; Score 378.5; DB 1; Length 695;
Best Local Similarity 21.8%; Pred. No. 7.6e-18;

Matches 166; Conservative 81; Mismatches 227; Indels 293; Gaps 35;

QY 137 GQILL-----ESYLNHCWETTHAKPGFVIOLEFWMLEFPMCOYDVEVDGNDRG 192
DB 27 GEILSPNYPAYEMEMKTDIEVEGFGVRLYFTLDMELSENCEYDSVOISGVEEG 86
QY 193 QIIKRVGNERP-----API-----QSIGSLHVLPHSDGS--KNPDGPHALY-----EET 237
DB 87 -----RLCGQRTSKANSPIVEEFOIPYKQLOVIFRSDFSNEERTGPAAYAAIDVNECT 142
QY 238 ACSSSPCFHDGTCVLDKAGSYKACLAGY----- 266
DB 143 DFTDVPESHFCNNPI-----GGYFCSCEPEYFLHDMRCVNGSGNVFTALIGHSNPY 199
QY 267 -----TGQRCN--LLEP-----RNCSDP----- 283
DB 200 NPYENSRCYQILLEGFQVNVTTIQREDFVEPADSQNCODSLFPAKRNQFGPFCGN 259
QY 284 ----- 297
DB 260 GFPGPLTIETHNTLDIVFTDLEQKKMKLRHYHGPIPCPEKITANSVMAPEKAYVF 319
QY 298 -----GLINGRAHAKIGTVVFFCNSNYLVSGNEKRTCOQNGEMSGK-----OPICIAKR 347
DB 320 KDVAKISCVDGFEAVENGVSTFFYS-----TCQSGQMSNRRLACQV---DCG 366
QY 348 EPKISDLVRRRVLPMQVSRTEPLHQLYSAFSKQKLSAPTKKPALPFGDLPMGYOHL 407
DB 367 IPE-----PIQNGKADDPDENTLFGSV----- 387
QY 408 TQLOVEGISPFY-----RLGSSRRTCILRTKWSG-----RAPGCIPICGKLENTAPKQ 458
DB 388 --IHSCEBPYYMEHAHGEGER--CANAGSWNDELIGIELPKCVPGV-----VPTG 437
QY 459 GLRWPMQALYRTSGVHDSLHKAGV-----FLVCSGALVNERTVVAHCVTDLGKVT 513
DB 438 PFR-----IQRIIFGGFPAKIQSFPMQVFEFFPRAGALIGEMVLTAAHVAGNDSP 491
QY 514 M-IKTADLVKLVLFKFRDDEKTIQSLQISAIILHPNDP-----ILLDADIALK 565
DB 492 MYVQSTSVRM-----ENLANVQKLTTRDVIILHPGWKPGDLSLSTRFPDIALVR 541
QY 566 LLDKARISTVQPICLAASRDLSTSPQESH---ITVAGW-----NVLADVRSRGFKNDT 616

DB 542 LKDPVVMGTVSPICLPRT---SSREPEBGLGISGGRERRNIVQLR----- 590
QY 617 LRSGVSVVDSJ-----LCEQHEHGIPLVSTDMNFCASWEPPTASDICTAETGIAAV 671
DB 591 ----GALPLTSLKCKQVKEENPKARADYVFTSMNICAGEKGV---DSCQDSSGAFPL 644
QY 672 SFFGRASPEPRNHLNGLVSWYDTCSSHRLSTAFKVLFPKQWIERBNK 720
DB 645 PVFN--VRDPKPYVAGLVSMG--KKCG--TYGIYTKVKNVYKDWIQTQ 687

RESULT 7

polyprotein - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C/Accession: T30337

R/Yang, J.C.; Lindsey, L.L.; Hedrick, J.L.

Submitted to the EMBL Data Library, March 1998

A/Description: cDNA cloning of ovocytinase, a chymotrypsin-like protease released from X

A/Reference number: Z20829

A/Accession: T30337

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1524 <YAN>

A/Cross-references: UNIPROT:Q91674; UNIPARC:UPI00000FBA76; EMBL:U01290; NID:G9291640; P

C:Superfamily: tyrosin related polyprotein; trypsin homology

Query Match 9.0%; Score 354; DB 2; Length 1524;
Best Local Similarity 22.3%; Pred. No. 8e-16;

Matches 166; Conservative 101; Mismatches 260; Indels 216; Gaps 39;

QY 55 CEKREVVGY-----TIPCCRNENECDSCLHPGCTIFENCKSGNMGWGLDFFYK 109
DB 214 CHAVLEPIHPLVDLDMLCAGFPEGMDACQDSSGSPF--CR--RSQW-----FLA 263
QY 110 GFYCAE---CRAGW-----YGDQMCQGYLRAP 135
DB 264 G--CVSMGLGCRSMWAKQIIRSQSGPAIFRSVSLDPLRPKLTGCGSSKGRITTK 321
QY 136 KGOI---LLESYPLNHCWETTHAKPGFVIOLEFWMLEFPMCOYDVEVDGNDRG 192
DB 322 NGTVRYPLSGNYSINSCWMLAVQAKTIERFQLOLDEHATCTFDLSFTVNE--- 377
QY 193 QIIKRVGNERPAPIQSIGSSSLHVLPHSDGSKNPDGFHAIVEIETACSSSPCFHDGTCV 252
DB 378 KMIRKVCSTISPLVIRSNKTYVTFSDGTGKGFELQFLAIPRKASAC--GSAKL 435
QY 253 DRAGSYKACLAGYTGQRCENLLEERNCSDP-----GGPVNGYQKITGGGGLIN 301
DB 436 KKKG-----MISPNYPDPYRLTKCSMIIEAPENHIVLKFEDFNVE 478
QY 302 GHRAKIGTVVFFCNSNYLVSGNEKRTCOQNGEMSGKQICIKACEKPIISLVLR---R 358
DB 479 YHGCTIYDAE-----YDGAEEK-----OLIAELCGY 506
QY 359 VLEPMQVSR-----TPLHQLYSAFSKQKLSAPTKKP--ALPFGDLPMGYOHLHQ 409
DB 507 TLPLPISSPENMLIRFKTIDMENSYPG--FKYKFSVPEKQPSLPVDYDPT--ISLHNR 563
QY 410 ---LOVEGISPFYRLGSSRRTCILRTKWSGKAPSCIP--ICGKIENITAPKTOGLRWPMQ 465
DB 564 AIALDVCGMAFM-----TPKV-----WLPRIYGGEE--ASPNS---WPMQ 598
QY 466 AAI--YRTSGVHDSLHKAGVFLVCSGALVNERTVVAHCVTDLGKVTMKTAD---LK 521
DB 599 VOIFLURT-----FH-----CEGALISPMWILTAHC-----IRAESPWT 635
QY 522 VVLGKFPYRDDR--DEKTIQSLQISAIILHPNDPILLDADIALKLDKARISTVQPI 579
DB 636 VLAG-----DHNNMLNSTEQINIKIRIHDVYNSTYNDIALLVLEPDLNDVVRV 691

QY 580 CLASRLSTSFQSHITVAGWVNLADVRSFGFKNDLTRGQVSVVDLSLCEQEDHGI 639
 ||| : : : : :
 Db 692 CLPEPEVLRT--PASVCVTVGMGNTADGGPALGLQQLQ---LPIIDSLICNTSYSG-- 744
 : : : : :
 QY 640 PVSTIDMFCASMEPTLPSPDICTAETGIAAVSFPGASPEPRKMLMGLVMSYDKTCSH 699
 : : : : :
 Db 745 --ELTDHMLCAGFPSSKEXKACQSDSGPLVCQ-----NEKEQPSIGLVSMWG--BQCG- 794
 : : : : :
 QY 700 RLST--AFTKVLPEKDWIERMK 720
 ||| : : : : :
 Db 795 RVSKRGVYTKRLEFPTMIQNTQ 817
 : : : : :

RESULT 8

JC6554
 Complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 05-Dec-1998 #sequence, revision 05-Dec-1998 #text_change 09-Jul-2004
 C/Accession: JC6554
 R/Sakai, H.; Nakashima, S.; Yoshimura, S.; Nishimura, Y.; Sakai, N.; Nozawa, Y.
 Gene 209, 87-94, 1998
 A>Title: Molecular cloning of a cDNA encoding a serine protease homologous to complement
 A:Reference number: JC6554, MUID:98192519, PMID:9524231
 A:Accession: JC6554
 A:Molecule type: mRNA
 A:Residues: 1-694 <SAK>
 A/Cross-references: UNIPROT:O70542; UNIPARC:UPI000066CA8; DBJ:DB8250; NID:g3080541; PT
 C:Comment: This protein is involved in glial cell differentiation and cartilage remodeling
 C:Genetics:
 A:Gene: r-gsp
 C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
 C:Keywords: differentiation; glycoprotein; hydrolase; serine proteinase
 F:1-21/Domin: signal sequence #status predicted <SIG>
 F:17-133/Domin: C1r/C1s repeat homology <C1R>
 F:22-694/Product: serine protease homolog #status predicted <MAT>
 F:111-177/Domin: EGF homology <EGF>
 F:300-360/Domin: complement factor H repeat homology <FHR>
 F:444-681/Domin: tryptsin homology <TRY>
 F:180,412/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:481,535,637/Active site: His, Asp, Ser #status predicted

Query Match 8.6%; Score 340.5; DB 2; Length 694;
 Best Local Similarity 21.2%; Pred. No. 2,76-15;
 Matches 167; Conservative 98; Mismatches 244; Indels 277; Gaps 40;

QY 44 ECGYDIOECVCPKRE-----VGYIIPCCR-----NEE----- 73
 ||| : : : : :
 Db 69 ENCAIVSVQITSGGIEERLCGRSSKSPNPTVEEFQFPYKRLQVFTSDFSNEERPTG 128
 : : : : :
 QY 74 -----NECDSCLIHPGCTIFENCKSCRNKSGWGTLLDPYKGFYCAECRAWYGG 123
 : : : : :
 Db 129 FAAYSAVDVNECTDFTDVF--CSHF-----CNN-----PIGGVFGS--CPPEYFLH 171
 : : : : :
 QY 124 DCNR-----CGQVLRAKQGLLES---YPLNAHCWTHAKRGVYQLRPMWLSLEF 173
 : : : : :
 Db 172 DDMRTCGVNCSGDVFTHALIGIASPNVNPYPENSRCYQLRQGF--RLVLTIRRRDF 229
 : : : : :
 QY 174 DYMCQYDVVEVRDGDNR-----DQQLIKRVCGRNRPAP--IQSGSLHVLPHSDG 222
 ||| : : : : :
 Db 230 D-----VEPADSEGNCHDSLTPAAKKQQRPGYCGNCFPPPLTIKTQSNLTLDIVFYDL 282
 : : : : :
 QY 223 SKNEDGFHALY-----EETITACS-----SSPCFHDGTCVLDAKASYSKACIAGYTG 268
 : : : : :
 Db 283 TGQKQKWLRYHGDPIPCPKELISANSIWEPKAKYVFD-----VVKITC----- 327
 : : : : :
 QY 269 QRCENLBERNCSDBGPGVNGYQKITGGPGGLNGRHAKITGVVAFPCNNSVYLSGNEKRT 328
 : : : : :
 Db 328 -----VDGFEEVVEGNVG-----STSFY-----ST 346
 : : : : :
 QY 329 CQONGEMSGK---OPICIKACREPKISDLVRRRLVPMQVQSRERPLHQLYSAAPSKQL 384
 ||| : : : : :
 Db 347 CQSNQGSNSRLKCPQV--DCGVPE-----PIENGKVEDPEDTEVGSV----- 387
 : : : : :

QY 385 QSAPTKKPALPFGLDPMGQHLHTLOQYECISPFY--RRIGSSRRITCLRTGKMSG----- 437
 : : : : :
 Db 388 -----IHYTCEBYYYMEQEEGGEHYCAANGSVVNNQGLV 422
 : : : : :
 QY 438 RASCTPICG-----KIEN--ITAPKTOGLRMPQAAIYRRTSGVHDSLHKAMFLVC 489
 : : : : :
 Db 423 ELKPCIPVCGVPEPRKVDQRIFGYSTKIQSPFMQVFEPSRPG----- 467
 : : : : :
 QY 490 SGALVNERITVVAHACVT--DLGKVTMIKTADLKLVVLGKFRDDDRDEKTIQSLQISAITL 548
 ||| : : : : :
 Db 468 -GALIDBYWVLTAAHVVEGNSDPWMTVGSTLKI-----EKLRNAQRLITERVII 516
 : : : : :
 QY 549 HPNYDP-----ILLADIALIKLDKARISTRVOPICLASRLSTSFQESH1--TV 598
 ||| : : : : :
 Db 517 HPSMKQEDDLNTRTNFDNDIALVQLDPMGMPTVAPICLP---ETFSQVNPSEVDLGLI 573
 : : : : :
 QY 599 AGNNVTLADVRSPPFKNDLTRGQVSVVDLSLCF---EQEDHGIYSTVTDNMFCASMEP 654
 : : : : :
 Db 574 SGWG-RTEIRITVNIQ---LRGAKLPITSLEKCCQGVNENPKARSNDVFTDNMICAGEKG 629
 : : : : :
 QY 655 TAPSDICTAETGIAAVSFPGRASPEPRKMLMGLVMSYDKTGSHRLSTAFKVLPEPKDW 714
 : : : : :
 Db 630 V---DSCEGDSGGAFLPVPN--VKDPKRTVAGLVSMG--KKCG--TYGIYTKVKNYVDM 680
 : : : : :
 QY 715 IERNMK 720
 ||| : : : : :
 Db 681 ILKTMQ 686
 : : : : :

RESULT 9

C1HNS
 Complement subcomponent C1s (EC 3.4.21.42) precursor [validated] - human
 N/Alternate names: C1 esterase precursor
 C/Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence, revision 31-Mar-1992 #text_change 09-May-2004
 C/Accession: A40496; A27381; S00224; S26732; S05634; A05140; A25396; A38407; B37820
 R/Kusunoto, H.; Hirosewa, S.; Sallier, J.P.; Hagen, F.S.; Kurachi, K.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7307-7311, 1988
 A>Title: Human genes for complement components C1r and C1s in a close tail-to-tail array
 A:Reference number: A40496; MUID:89017187; PMID:24559702
 A:Accession: A40496
 A:Molecule type: mRNA
 A:Residues: 1-688 <KUS>
 A/Cross-references: UNIPARC:UPI0000126BF6; GB:J04080; NID:g179645; PIDN:AAA51852.1; PID
 R/Iosi, M.; Duponchel, C.; Meo, T.; Jullier, C.
 Biochemistry 26, 8516-8524, 1997
 A>Title: Complete cDNA sequence of human complement C1s and close physical linkage of C1
 A:Reference number: A27381; MUID:88163522; PMID:2831944
 A:Accession: A27381
 A:Molecule type: mRNA
 A:Residues: 1-688 <TOS>
 A/Cross-references: UNIPARC:UPI0000126BF6; GB:M18767; NID:g179647; PIDN:AAA51853.1; PID
 R/Mackinnon, C.M.; Carter, P.E.; Smyth, S.J.; Dunbar, B.; Fothergill, J.E.
 Eur. J. Biochem. 169, 547-553, 1987
 A>Title: Molecular cloning of cDNA for human complement component C1s. The complete ami
 A:Reference number: S00224; MUID:88082788; PMID:3500856
 A:Accession: S00224
 A:Molecule type: mRNA
 A:Residues: 1-688 <MAC>
 A/Cross-references: UNIPARC:UPI0000126BF6; EMBL:X06596; NID:g29542; PIDN:CAA29817.1; PI
 A:Accession: S26732
 A:Molecule type: protein
 A:Residues: 16-38;68-116;170-236;246-262;265-280;282-284;287-308;315-363;384-394;421-43
 A/Cross-references: UNIPARC:UPI000015033A; UNIPARC:UPI00000172BCD; UNIPARC:UPI00000172BCE
 BD3; UNIPARC:UPI0000172BD4; UNIPARC:UPI0000172BD5
 R/Iosi, M.; Duponchel, C.; Meo, T.; Couture-Tosi, E.
 J. Mol. Biol. 208, 709-714, 1989
 A>Title: Complement genes C1r and C1s feature an intronless serine protease domain clos
 A:Reference number: S05634; MUID:90040704; PMID:2553984
 A:Accession: S05634
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 356-513, 'G', 514-688 <TO2>

137 GQTL-----ESYPLNAHCWTHAKPGFVQLRFLVWLSLEFDYMCQDYDVEVADGDRDG 192

Db 21 GELISPNYQAVYBEVEKSNMIDIEVREGGHLHYTHLIDIEISEKCAVDSQIISGDIIEEG 80
Qy 193 QIIRKVCAGNERPADI-----QSIGSLHVLPHSDGS--KNFDGFAIY--EETIACS---S 241
Db 81 RLCCGRSSNNPHSDIIVEFQVPYKYLQVIFKSDPSNEREFQFAAYVATDINCTGFVD 140
Qy 242 SPCHDGTCTVLDKAGSKKCACTAGY----- 266
Db 141 VPCHFPCNNFI---GGYFSCSPPEYFLHDMKNCVNGSGDVFTALIGELASPNYPRYP 197
Qy 267 TGQSCENIL-----BEKNCSD-----PGGVNGYQKIT 294
Db 198 ENSKCEQIRLEKGFQVVYTLRRDFVEADASAGNCLDSLVFVAGDRQGFPGYGH--- 253
Qy 295 GGPGLIN-----GRHAK--I 307
Db 254 GFPEPLNIFETKSNALDIIIFQTLTGQKKMKLIRHSDPMCPKEDPTNSWEPKAKAYVF 313
Qy 308 GTVVSFFCNSNY-VLSG-----NEKTCQONGEWGSK---QPICTACREPKISDLVR 357
Db 314 RDVVQITCLDGFVEVEGRVGATSFYSYCSQSGKMSNKLKQAPV---DCGIP----- 362
Qy 358 RVLNQVQSRRETFPLHOLYSAAFSKQYQSAPTKRP-ALPRGDLPMGYQHLTQIQYECIS 416
Db 363 -----ESIENGVEDPESTLFGSV-----IRYCEE 388
Qy 417 PFY---RLIGSSRRTCLRTGKWSGRA-----PSCIPIGKIENITAPKTQGLRPMQOAIY 469
Db 389 PYTMENGGGGEHYCAAGNSWNEVLQELPKCYVCG-----VP-----REFPEEK-- 435
Qy 470 RRTSGVHDGSLHKAMFLVY---CSGALVNERTVVAAHCVTDLGKVTMKTADLRVL 524
Db 436 QRIIGSGDADIKNPFMQVFEQNPWAGALLINEYVTLAAHVEGNREPTM-----YV 487
Qy 525 GKFRDDDRDEKTIQSIQISAIILHENVDPILL-----DADIALLKLDKAISTRVQ 577
Db 488 GSTSVQTSRLAKS--KMLTPBEVFIHPGMKLLVEBEGRTNPFNDIALVRLQDPVKGPTVS 546
Qy 578 PICLAASRDISTFSQESHITVAGNNVLADVSPQEKND---TLRSQVSVSDSLCEBQH 634
Db 547 PICLPGRSSDYNDMLDGLISGNG---RTE--KEDRAVRLQAARLPVAPLAKCKEYK 599
Qy 635 EDHGIPVS-----VTDNMFCASWEPPTAPSDICTAETGGIAAASVFPGRASPEPRMHLML 688
Db 600 VEK---PTADAAAYVFTPRMIGAGE--KMDSCSGDGGGANAAYQDP---NDKTFYAAGL 652
Qy 689 VSMISYDKTCSHRLSTAFKVLPEKWIERNKK 720
Db 653 VSMG--PQCG--TYGLYTRVKNVYDMINKTQ 680

RESULT 10
A:Accession: A56318
A:Residues: 1-1019 <KIT>
N:Alternate names: enterokinase
C:Species: Homo sapiens (man)
C:Date: 19-May-1995 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C:Accession: A56318; B43090
R:Kittamoto, Y.; Velle, R.A.; Donis-Keller, H.; Sadler, J.E.
Biochemistry 34, 4562-4568, 1995
A:Title: cDNA sequence and chromosomal localization of human enterokinase, the proteolytic
A:Reference number: A56318; MUID:95234679; PMID:7718557
A:Accession: A56318
A:Molecule type: mRNA
A:Residues: 1-1019 <KIT>
A:Cross-references: UNIPROT:P98073; UNIPARC:UPI000003FE65; GB:U09860; NID:G746412; PIDN
R:Kittamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A:Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compo
A:Reference number: A43090; MUID:94329561; PMID:8052624
A:Accession: B43090
A:Status: nucleic acid sequence not shown

A/Molecule type: mRNA
A/Residues: 749-1019 <K12>
A/Cross-references: UNIPARC:UPI0000172B0B; GB:U09860
C/Comment: The mechanism of association with the membrane of the intestinal brush border (located below) or with amino-terminal myristoylation of the heavy chain.
C/Genetics:
A/Gene: GDB:PNSS7
A/Cross-references: GDB:384083; OMIM:226200
A/Map position: 21q21-21q21
C/Complex: Mature enteropeptidase is variously reported to contain two (heavy and light) ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involves a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involves a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involves a disulfide bond.
C/Function:
A/Description: cleaves activation peptide from trypsinogen to produce active trypsin
A/Pathway: intestinal digestive hydrolase cascade
C/Superfamily: enteropeptidase; Ctr/Cts repeat homology; LDL receptor ligand-binding repeat
C/Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen
F/1-784/Product: enteropeptidase heavy chain #status predicted <HCH>
F/12-38/Domain: transmembrane #status predicted <TM>
F/164-221/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F/342-504/Domain: MAM homology <MAM>
F/526-631/Domain: Ctr/Cts repeat homology <CTR>
F/643-677/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F/678-783/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC>
F/785-1019/Product: enteropeptidase light chain #status predicted <LCH>
F/785-1019/Domain: trypsin homology <TRY>
F/116,147,179,328,388,440,470,503,534,630,682,706,725,848,887,909,949/Binding site: F/772-896,810-826,910-977,941-956,967-995/Disulfide bonds: #status predicted
F/825,876,971/Active site: His, Asp, Ser #status predicted

Query Match 8.4%; Score 331.5; DB 1; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.7e-14;
Matches 136; Conservative 90; Mismatches 225; Indels 143; Gaps 27;

QY 143 SYPLNACEWTHAKRGFVQLRFLVMSLEFDVWQDYVYVRRGDNRRDGIIRKVCNE 202
DB 545 SYPLNACEWTHAKRGFVQLRFLVMSLEFDVWQDYVYVRRGDNRRDGIIRKVCNE 598
QY 203 RPAPISIGSSILH-----VLPHSDGSKNF-DGFHAIYEETITACSSPCFHDGCV 251
DB 599 -PGVKNVFFSTTNMTVLLINDVLARGFKNFTTGHILGIP-----PC----- 643
QY 252 LDKAGSYKC-----GYTGRCENLLEBRNCSDPGVNGYQKITGGPGLING 302
DB 644 --KADHQCCKNGECVPLVNLCDGHL--HCEGSDSEAD-----VRFNGTNNNGIARF 693
QY 303 RHAIIGTVVSFFCNSVYLSGNEKRTCOQNGEMSGKQPICTKACREPKISDLVRRVLP 362
DB 694 RIQSIW-----HTACAEWTTQIISNDVC-----QLIGLT 721
QY 363 QVGRREPLHQLVSAAFSKOKLOSAPTKKRALPGDLPNGYQHLHTOLOVECTSPYRRL 422
DB 722 GSSGSSKRIFFSTDGPF--VKLNTAHPD-----GHILTPSOQLDLSIRL 765
QY 423 GSSRRTLRTGKWSGRAPSCIPICGKIENITAPKTQGLRMPQAAIYRTSGVHDSLHK 482
DB 766 QCNHKS-----GKTLAADIPIKTI--VGSNAKEGAMPWVGLY-----YGR-- 807
QY 483 GAWLVSGALVNERTVVAACHCTDGLKTMITADLKVVLGKFRYDDDEKTIQSLQ 542
DB 808 ---LTCGASLVSSDMLVSAHCV--YGR--NLEPSKMTALIGLHMSKNLSPQVPL 858
QY 543 ISAIILHNVPDILDLADIILKLDKARISTRVOPICLAASRDLSFSOSHITVAGWN 602
DB 859 IDELVINPHYRRKNDIAMHLEFKNYTDYIOLIPLENOVFPFGR--NCSIAWG 916
QY 603 VLADVSPGFKNDTLRSVSVVSDLLCEQHEHDSIPVSVYDNNMFCASWEPASPDICT 662
DB 917 T---VVVGGTANTILQEDAVPLLSNERCQCMPEX---NITEMNICAGYE-BEGIDSCQ 968
QY 663 AETGGAIAVSPFGAASPERRHLMLGLVMSYDKTCSHSLSTAFKVLVLPFKWIE 716
DB 969 GDSGG-----PLMCOENNRWFLAGVTSFGYKCALPNR-PGVYARVSHFTMIQ 1015

RESULT 11

A53663
enteropeptidase (EC 3.4.21.9) precursor (validated) - pig
N/Alternate names: enterokinase
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 07-Oct-1994 #sequence_revision 09-Aug-1996 #text_change 28-Apr-2003
C/Accession: A53663
R/Matsuura, M.; Ichinose, M.; Yahagi, N.; Kakai, N.; Tsukada, S.; Maki, K.; Kurokawa, J. Biol. Chem. 269, 19976-19982, 1994
A/Title: Structural characterization of porcine enteropeptidase.
A/Reference number: A53663; MUID:94327548; PMID:8051081
A/Accession: A53663
A/Molecule type: mRNA
A/Residues: 1-1034 <MAT>
A/Cross-references: UNIPARC:UPI0000172B0C; GB:D30799; NID:G505122; PIRN:BA06459.1; PID
A/Note: parts of this sequence, including the amino ends of three chains isolated from t
C/Comment: The mechanism of association with the membrane of the intestinal brush border (located below) or with amino-terminal myristoylation of the heavy chain.
C/Complex: Mature enteropeptidase is variously reported to contain two (heavy and light) ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involves a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involves a disulfide bond.
C/Function:
A/Description: cleaves activation peptide from trypsinogen to produce active trypsin
A/Pathway: intestinal digestive hydrolase cascade
C/Superfamily: enteropeptidase; Ctr/Cts repeat homology; LDL receptor ligand-binding repeat
C/Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen
F/12-38/Domain: transmembrane #status predicted <TM>
F/52-117/Product: enteropeptidase mini chain #status predicted <MCH>
F/118-799/Product: enteropeptidase heavy chain #status predicted <HCH>
F/159-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F/357-519/Domain: MAM homology <MAM>
F/541-646/Domain: Ctr/Cts repeat homology <CTR>
F/568-692/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F/683-798/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SR>
F/800-1034/Product: enteropeptidase light chain #status predicted <LCH>
F/800-1034/Domain: trypsin homology <TRY>
F/116,147,170,194,283,343,350,403,455,485,518,549,645,697,701,721,740,761,804,863,902,9
F/787-911,825-841,925-992,956-971,985-1010/Disulfide bonds: #status predicted
F/840,891,986/Active site: His, Asp, Ser #status predicted

Query Match 8.4%; Score 330.5; DB 1; Length 1034;
Best Local Similarity 22.9%; Pred. No. 2e-14;
Matches 137; Conservative 86; Mismatches 224; Indels 151; Gaps 27;

QY 143 SYPLNACEWTHAKRGFVQLRFLVMSLEFDVWQDYVYVRRGDNRRDGIIRKVCNE 202
DB 560 NYPQAFQVWNLNAQKKNLQLHFE---EFLENIADVVEIRDGEDSLLAVYTG-- 613
QY 203 RPAPISIGSS---LHVLPHSDS-----KNF-DGFHAIYEETITACSSPCFHD--- 247
DB 614 -PGVEDVFFSTTNMTVLLFTNDALTKGFKANFTTGHILGIP-----PKEDNFOC 665
QY 248 --GTCVLDKAGSYKCAAGLYTGRCENLLEBRNCSDPGVNGYQKITGGPGLINGRNA 305
DB 666 ENGEICVL-----LVNLCDGFSHGCDGSDBAHCVAFLNGTANNSGLVGRRIQ 711
QY 306 KIGTVVSFFCNSVYLSGNEKRTCOQNGEMSGKQPICTKACREPKISDLVRRVLP 365
DB 712 SIW-----HTACAEWTTQTSDDVC-----QLIGLTG 729
QY 366 SRETPPLHQLVSAAFSKOKLOSAPTKKRALPGDLPNGYQHLHTOLOVECTSPYRRLGSS 425
DB 740 NSSMFPFSSGGGPF--VKLNTANGSILTASE-----QCEBDSLILQCN 763
QY 426 RRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLR-----WPOAAIYRTSGVHDS 479
DB 784 HKSC---GK-----KQVAGVSPKIVGSDRSRGAMPVVALY-----YNGQ 822
QY 480 LHKGAWLVSGALVNERTVVAACHCTDGLKTMITADLKVVLGKFRYDDDEKTIQ 539
DB 823 ---LTCGASLVSSDMLVSAHCV--YGR--NLEPSKMTALIGLHMSKNLSPQVPL 870

QY 540 SLQISAIIHPNYPILLDADIALKLKDKARISTREVOPICLAASRLSTSPQESH-ITV 598
 Db 871 TRILIDIVINPHNRKRKSDIMMHLFEKVTYTDYIQPICLPEENOV---FPPGRICST 927
 QY 599 AGNNVLADYRSPGKNDTLRSVVSDSLICEQHDHGI PVSVTDNMFCASMEPTAPS 658
 Db 928 AGMKVYIYGSPA---DIIGADVPLISNKKCOQMPREY---NITENMNCAGYE-EGGI 979
 QY 659 DICTATGCGIAAVSPGRASPEPRMHLMGVSWSYDKTCSHRLSTAFKYLPRKDWIE 716
 Db 980 DSCQDSGG-----PLMCLENNRMWLLAGVTSFGYCALPNNR-PGVYARVPKFTWITQ 1030

RESULT 12

QX0210
 protein C (activated) (EC 3.4.21.69) precursor - mouse
 N/Alternate names: vitamin K-dependent serine proteinase
 C/Species: Mus musculus (house mouse)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: JX0210
 R/Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
 J. Biochem. 111, 491-495, 1992
 A/Title: Isolation and characterization of a mouse protein C cDNA.
 A/Reference number: JX0210; MUID:92316897; PMID:1618739
 A/Accession: JX0210
 A/Molecule type: mRNA
 A/Residues: 1-461 <TAD>
 A/Cross-references: UNIPROT:P33587; UNIPARC:UP100000278D0; GB:D10445; NID:G220385; PIDN:
 A/Experimental source: liver
 C/Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
 s.
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F/1-33/Domain: signal sequence #status predicted <SIG>
 F/27-85/Domain: Gla domain homology <GLA>
 F/34-41/Domain: propeptide #status predicted <PRO>
 F/121-196/199-461/Product: protein C #status predicted <PRC>
 F/42-196/Domain: light chain #status predicted <PCL>
 F/91-130/Domain: EGF homology <EG1>
 F/139-174/Domain: EGF homology <EG2>
 F/199-461/Domain: heavy chain #status predicted <ACT>
 F/212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>
 F/212-445/Domain: trypsin homology <TRY>
 F/47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F/112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F/121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat
 F/214,290,355/Binding site: carboxylate (Asn) (covalent) #status predicted
 F/253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 8.14; Score 320; DB 1; Length 461;
 Best Local Similarity 23.94; Pred. No. 4.2e-14;
 Matches 145; Conservative 70; Mismatches 174; Indels 218; Gaps 29;
 QY 152 WTI-----HAKPF-----VIQLFVWLSLEFDYMCQYDVYVAVDGNRGOIIRV 198
 Db 14 WGISSTPAHPDPVFSSEHAHQVLRVRANSFLE-----EMRPG-SLEKCEKEI 62
 QY 199 CGNERPAPI-QSIGSLHVLFSHSGSNFPGFPAIYEITACSSSPCFHGTGTVLDKAGS 257
 Db 63 CDPEAEQETIQNVNEDTLAFWI-----KTFBDQCSAPPLDHQCDSPCCGCTCT-DSIGS 116
 QY 258 YKCACTAGTQGRCENLLEERNCSDDPGAPVNGYQKITGPGRL-----INGRAKIGTVV 311
 Db 117 FSCSCDKMGEGKFCQQLRFQDC-----RVNNGGCLHYCLEESNGRCA----- 160
 QY 312 SFQNNNSYVLSNMEK-----TCQNGEMSGKQPICTICACREPKSLDVRVRVLMQV 364
 Db 161 ---CAPGYELADDMRKSTVNFPGGLGRITER-----KKRIL----- 196
 QY 365 QSERETPLHQLYSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAF 424
 Db 197 -KNDTDL-----EDLEPPD----- 210

QY 425 SRRTCLRTGKMGSRAPSCIPICGKIENITAPKTQGIIRWQOAIYRTSGVHDSJLHKA 484
 Db 211 -----RYNGTILTK-QG-DSPWOAILL-----DSKCK-- 235
 QY 485 WFLVSGALVNERVTVAACVTDLGKVTMKTADLKVYLGRFYRDDDEKTIQSLQIS 544
 Db 236 --LACGVLITHSWVLTAAHCVBGTKKL-----VRLGEY--DLRRRDHEDLDLTK 283
 QY 545 AIILHPNYPILLDADIALKLKDKARISTREVOPICL-----AASRLSTSPQESHITVAG 600
 Db 284 EILVHPNTRSSDNDIALRLAQPATLSKTIPIPLPNNGLAQSLTQAGETVVT--G 341
 QY 601 WNVLADYRSPGKNDTL-----RSVVSDSLICEQHDHGI PVSVTDNMFC 649
 Db 342 WGYOSDRIDKGRNRFTILFTIRIPLVANECVEVWKNV-----VSENMLC 387
 QY 650 ASMEPTAPSDICGAETGIAAVSPGRASPEPRMHLMGVSWSYDKTCSHRLSTA-FTKY 708
 Db 388 AGIIGNT-RDACCDSGGGPMVVFRRG-----TWFLVGLVSWG--EGCGHTNNGIYTKV 438
 QY 709 LPEKDWI 715
 Db 439 GSYLKKWI 445

RESULT 13

A43090
 enteropeptidase (EC 3.4.21.9) precursor [validated] - bovine
 N/Alternate names: enterokinase
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: A43090; A48874; A61436
 R/Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
 Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
 A/Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease comp
 A/Reference number: A43090; MUID:94339561; PMID:8052624
 A/Accession: A43090
 A/Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1035 <KIT>
 A/Cross-references: UNIPROT:P98072; UNIPARC:UP1000004BBB5; GB:U09859; NID:g746410; PIDN
 A/Experimental source: small intestine
 R/Lavallie, E.R.; Rehmertulla, A.; Racie, L.A.; DiBlasio, E.A.; Ferenz, C.; Grant, K.L.;
 J. Biol. Chem. 268, 23311-23317, 1993
 A/Title: Cloning and functional expression of a cDNA encoding the catalytic subunit of
 A/Reference number: A48874; MUID:94043122; PMID:8226855
 A/Accession: A48874
 A/Molecule type: mRNA
 A/Residues: 801-1035 <LAV>
 A/Cross-references: UNIPARC:UP100001133D; GB:D19663; NID:g416131; PIDN:AAAL6035.1; PID
 A/Note: parts of this sequence, including the amino end of the mature protein, were con
 J. Light, A.; Janaka, H.
 J. Protein Chem. 10, 475-480, 1991
 A/Title: The amino-terminal sequence of the catalytic subunit of bovine enterokinase.
 A/Reference number: A61436; MUID:92189715; PMID:1799406
 A/Accession: A61436
 A/Molecule type: protein
 A/Residues: 801-807, 'Y', 809-827 <LIG>
 A/Cross-references: UNIPARC:UP100001468A0
 C/Comment: The mechanism of association with the membrane of the intestinal brush border
 embryo attachment using a signal-anchor sequence.
 C/Comment: Conversion from membrane-bound to soluble forms may involve further processi
 C/Complex: mature enteropeptidase is variously reported to contain two (heavy and light)
 lide linked
 C/Function:
 A/Description: cleaves propeptide from trypsinogen to produce active trypsin
 A/Pathway: intestinal digestive hydrolase cascade
 C/Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding re
 C/Keywords: glycoprotein; hydrolase; intestine; serine proteinase; transmembrane protei
 F/22-38/Domain: transmembrane #status predicted <TM>
 F/52-117/Product: enteropeptidase mini chain #status predicted <MC>
 F/118-800/Product: enteropeptidase heavy chain #status predicted <HC>

Db 436 TYFVTGIVSWG--EGCARKKYGVYTKLSRFLRWVTVNR 473

RESULT 15

JC7731

membrane-bound arginine-specific serine proteinase precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: J07731, J07775

R:Kishi, K.; Yamazaki, K.; Yasuda, I.; Yahagi, N.; Ichinose, M.; Tsuchiya, Y.; Athauda, J. Biochem. 130, 425-430, 2001

A:Title: Characterization of a membrane-bound arginine-specific serine protease from rat

A:Reference number: J07731, NCID:21421307; PMID:11530019

A:Accession: J07731

A:Molecule type: mRNA

A:Residues: 1-855 <RIS>

A:Cross-references: UNIPROT:Q9JUT7; UNIPARC:UPI000008BAC0; DDBJ:AB049189

A:Experimental source: strain Male, 7-week-old

R:Satom, S.; Yamazaki, Y.; Tazuki, S.; Hitomi, Y.; Iwanaga, T.; Fushiki, T.

Biochem. Biophys. Res. Commun. 287, 995-1002, 2001

A:Title: A role for membrane-type serine protease (MT-SPI) in intestinal epithelial turn

A:Reference number: J07775; PMID:11573963

A:Contents: Small intestine

A:Accession: J07775

A:Molecule type: mRNA

A:Residues: 1-855 <SAT>

A:Cross-references: UNIPARC:UPI000008BAC0; DDBJ:AB037898

C:Comment: This enzyme, an epithelial-derived, type II integral membrane serine protease of specific proteins or peptides on the brushborder membranes. It also participates in

lial migration and/or cell loss.

C:Genetics:

A:Gene: mt-spi

A:Map position: basolateral cell surface

C:Superfamily: membrane-bound arginine-specific serine proteinase

C:Keywords: protein digestion

Query Match 7.9%; Score 313; DB 2; Length 855;

Best Local Similarity 21.4%; Pred. No. 2,4e-13;

Matches 151; Conservative 78; Mismatches 227; Indels 250; Gaps 33;

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QY 82 HRG--CTIFENCKSCNNGSWGTLDDPFYVGFCAECBAGWYGDDCMRCQGVLRAPKQI 139
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Db 324 HRGFETFFQLPKM---SSCGILSF--AQGTFFSP---YYPG----- 358
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 140 LIESYPLNHCENTHAKEGFIQLRFVMSLEFDYM---CQDYVEVARDGNDQI 195
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 359 ---HYPPINICTWNIKVPNNRNVKVPKLFYLDVPIPVGSCTKDYVEING----- 406
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 196 KRYCGERAPRPIOSIGSSSLHYLFHSDGSKNFDGFHAIYEITACSSSPC-----FHDGTC 250
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 407 EKFCGERSQFVVSNSSKITVHFHSDHSYDTGFLAEY--LSYSDNDPCGFMCKTGRC 464
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 251 VL-----DKAGSYKACLAGY-----TGRCENL-----EERNGS 281
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 465 IRKDLACDGAADCPDYSDEHRCNATHQPMCKNQPKPLFWCDVNDGDSDEGCS 524
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 282 DPGGPVNGYQKITGPGGLNGRHAIGTVVSPFCNNSSYVL---SGNEKRTCOQNBWSG 337
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 525 CPAG-----SFKCSNGKCLPQSQCGNKGDDCCGSDSEAS 558
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 338 KQPICTKACREPKISDLVRRRLVPMOVQSHREPLHQLYSAFSKQKIQSAPTKKPALPFG 397
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 559 CDNVNAVSC----- 567
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 398 DLPFGYQHLYTOLQYECISPFYRLGSSRRTCLRTGWSGRAPSCIPICGKINITAPKT 457
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 568 ---TKYTRC-----QNGCLCNKGN---PEC---DGKDCSDGSDE 599
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 458 Q-----GLR-----WPMQAIYRRTSGVHDSLHKAMFLVCSGLV 495
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 600 KNDCDGLRSFTKQARVVVGVTNADEGEWPMQVSLHALGQG-----H-----LCGASLIS 647
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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QY 496 BRTVVAAHCVTDLGKVTMIKTAD---LKVLGKFFYRDDRDDEKTIQSLQISATILHPNY 552
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 648 PMLVSAHACFOD---ETIFKISDHTMTATFLG-LLDGSKRSASGVQEHKRIITHPSF 703
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 553 DPLLDADIAIILKLDKARISTRVOPICLAASRDLSSTFQESHITVAGNNVLADVRSPGF 612
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 704 NDFTEVDYDIALLEKPAEYSTVVRPCLPDNTHVFPAKGA--IWTGW---GHTREGGT 758
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 613 KNDTLRSGVSVVDSILCEQHEHDGIPVSVTDNMFCSMEPTAFPSDICTAETG-IAAV 671
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 759 GALILQKGEIRVINOJTCEEL-----LPQOITPRMKCVGF-LSGGVDSQGDSPGLSSV 812
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 672 SPPGRASPEPRMHLMLGVSWSYDXTCSHRLST-AFTKVLPRDWIE 716
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 813 EKDGLI-----FQAGVSWG--EGCAQNNKPGVYTRLPVARDWIK 850
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

```

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Job time : 50 secs

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OM protein - protein search, using sw model
Run on: April 4, 2007, 21:58:01 ; Search time 221 Seconds
(without alignments)
1594.208 Million cell updates/sec

Title: US-10-063-546-38
Perfect score: 3945
Sequence: 1 MEIGCTQGLFPLQLLLIS.....LSTAPFKVLPEKDIERNKK 720
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 2782304 seqs, 48933398 residues
Total number of hits satisfying chosen parameters: 2782304
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV6695	standard;	protein;	720	AA.	
DE	Membrane-bound protein					PRO1344.
PN	WO963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 3;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;				
RESULT 2						
ID	AAU29108	standard;	protein;	720	AA.	
DE	Human PRO polypeptide sequence					#85.
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 4;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;				
RESULT 3						
ID	AA87544	standard;	protein;	720	AA.	
DE	Human PRO1344.					
PN	WO20016318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 4;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;				
RESULT 4						
ID	AA865218	standard;	protein;	720	AA.	
DE	Human PRO1344 (UNQ699) protein sequence					SEQ ID NO:231.
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 4;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;				
RESULT 5						
ID	ABG95869	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein					PRO1344.
PN	US2002119130-A1.					
PD	23-AUG-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 5;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;				
RESULT 6						
ID	ABUS8484	standard;	protein;	720	AA.	

DE	Human PRO polypeptide	#85.			
PN	US2003027272-A1.				
PD	06-FEB-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;	
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;			
RESULT 7					
ID	ABU86032	standard;	protein;	720	AA.
DE	Novel human secreted and transmembrane protein				PRO1344.
PN	US2003032127-A1.				
PD	13-FEB-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;	
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;			
RESULT 8					
ID	ABU84347	standard;	protein;	720	AA.
DE	Human secreted/transmembrane protein (PRO)				#85.
PN	US2003032112-A1.				
PD	13-FEB-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;	
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;			
RESULT 9					
ID	ABR66221	standard;	protein;	720	AA.
DE	Human secreted polypeptide				PRO1344, SEQ ID NO:170.
PN	US2003027278-A1.				
PD	06-FEB-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;	
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;			
RESULT 10					
ID	ABR65611	standard;	protein;	720	AA.
DE	Human secreted polypeptide				PRO1344, SEQ ID NO:170.
PN	US2003036159-A1.				
PD	20-FEB-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;	
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;			
RESULT 11					
ID	ABU99551	standard;	protein;	720	AA.
DE	Human secreted/transmembrane protein (PRO)				#85.
PN	US2003040070-A1.				
PD	27-FEB-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;	
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;			
RESULT 12					
ID	ABUS8033	standard;	protein;	720	AA.
DE	Human PRO polypeptide				#85.
PN	US2003027163-A1.				
PD	06-FEB-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;	
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;			
RESULT 13					
ID	ABU59111	standard;	protein;	720	AA.
DE	Novel human secreted or transmembrane protein				PRO1344.
PN	US2002132252-A1.				
PD	19-SEP-2002.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;	
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;			
RESULT 14					
ID	ABU82623	standard;	protein;	720	AA.
DE	Human secreted/transmembrane protein				PRO1344.
PN	US2003032023-A1.				
PD	13-FEB-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;	
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;			
RESULT 15					
ID	ABU82790	standard;	protein;	720	AA.
DE	Human PRO polypeptide				#85.
PN	US2003032113-A1.				
PD	13-FEB-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;	
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;			
RESULT 16					
ID	ABU89911	standard;	protein;	720	AA.
DE	Novel human secreted and transmembrane protein				PRO1344.
PN	US2003036147-A1.				

PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 17
ID ABR68160 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 18
ID ABU60542 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 19
ID ABU96213 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 20
ID ABU92644 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 21
ID ABO08721 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 22
ID ABO02773 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 23
ID ABR74927 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 24
ID ABR94689 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 25
ID ABU13924 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 26
ID ABR85662 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036140-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 27
ID ABU98822 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 28
ID ABU98037 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 29
ID ABU91743 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 30
ID ABU89436 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 31
ID ABU86277 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 32
ID ABU67490 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 33
ID ABU80518 standard; protein; 720 AA.
DE Human PRO protein #85.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 34
ID ABU72509 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 35
ID ABU90894 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 36
ID ABO33953 standard; protein; 720 AA.

DE Human secreted/transmembrane protein PRO1344.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 37
ID ABR99436 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 38
ID ABR98826 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 39
ID ABO16349 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 40
ID ABR92249 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 41
ID ABO18890 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 42
ID ABR78311 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 43
ID ABR71970 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 44
ID ABR85047 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 45
ID ABO00186 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 46
ID ABO11518 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 47
ID ABO02163 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 48
ID ABR8737 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 49
ID ABR83432 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 50
ID ABO06233 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 51
ID ABR59269 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 52
ID ABO09331 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 53
ID ABO19195 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 54
ID ABO11213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 55
ID ABR6831 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 56
ID ABO16044 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040060-A1.

PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 57
ID ABO13750 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 58
ID ABU71524 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 59
ID ABU65653 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, SEQ ID 170.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 60
ID ABO07501 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 61
ID ABO03568 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 62
ID ABR67136 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 63
ID ABO15739 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 64
ID ABU56020 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, PRO1344.
PN US2003022398-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 65
ID ABU72305 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 66
ID ABU65348 standard; protein; 720 AA.
DE Human secreted polypeptide #85.
PN US2003032102-A1.

PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 67
ID ABU95293 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 68
ID ABU71196 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 69
ID ABO07806 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 70
ID ABR70047 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 71
ID ABR69380 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 72
ID ABO01521 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US200308353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 73
ID ABU81323 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 74
ID ABR60120 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 75
ID ABU90978 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 76
ID ABR67855 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027269-A1.

PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 77
ID ABR65243 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 78
ID ABR6465 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 79
ID ABR7187 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 80
ID ABO59258 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 81
ID ABO8357 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 82
ID ABO89047 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 83
ID ABO83127 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 84
ID ABO94983 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 85
ID ABO90531 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 86
ID ABO84042 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 87
ID ABO93693 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 88
ID ABO25955 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 89
ID ABR64938 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 90
ID ABO27299 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 91
ID ABR68770 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 92
ID ABO06586 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 93
ID ABR99131 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 94
ID ABO57015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 95
ID ABO85967 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 96
ID ABO82254 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 97
ID ABU87265 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 98
ID ABU83737 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 99
ID AB008111 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 100
ID ABU92494 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 101
ID ABU81822 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 102
ID ABU65986 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 103
ID ABU81164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 104
ID ABR59815 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 105
ID ABU94003 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 106
ID ABU99856 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

RESULT 107
ID ABR65526 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 108
ID ABR90944 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 109
ID ABO53779 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 110
ID ABU58964 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 111
ID ABU94371 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 112
ID ABU79253 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 113
ID ABU86582 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 114
ID ABU8687 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 115
ID ABU94676 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 116
ID ABO04603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

RESULT 117
ID ABR70352 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 118
ID ABU92344 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 119
ID ABU98517 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 120
ID ABR65916 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036165-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 121
ID ABR64633 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 122
ID ABU59407 standard; protein; 720 AA.
DE Novel human secreted or transmembrane protein PRO1109.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 123
ID ABU79558 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 124
ID ABU92949 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 125
ID ABU95908 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 126
ID ABU91128 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 127
ID ABU90221 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 128
ID ABO09636 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 129
ID ABO10908 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 130
ID ABR70962 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 131
ID ABU98281 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183493-A1.
PD 05-DEC-2002.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 132
ID ABU87570 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 133
ID ABU91438 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 134
ID ABU89286 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036634-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 135
ID ABU84652 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 136
ID ABR69742 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 137
ID ABU80119 standard; protein; 720 AA.
DE Human PRO protein #85.

PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 138
ID ABR82493 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 139
ID ABR92173 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 140
ID ABR93388 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 141
ID ABO09941 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 142
ID ABO09026 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 143
ID ABR96457 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 144
ID ABR10879 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 145
ID ABR10594 standard; protein; 720 AA.
DE Human secreted/transmembrane protein #85.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 146
ID ABR81631 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 147

ID ABR72127 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 148
ID ABR95603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 149
ID ABR96812 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 150
ID ABR70657 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 151
ID ABO05008 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 152
ID ABO08416 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 153
ID ABR88570 standard; protein; 720 AA.
DE Human secreted and transmembrane polypeptide PRO1344.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 154
ID ABO34084 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 155
ID ABO05623 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 156
ID ABR74012 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

RESULT 157
ID ABR95604 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 158
ID ABR89901 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 159
ID ABR81206 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 160
ID ABM00902 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 161
ID ABR8504 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 162
ID ABM77325 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 163
ID ABO28809 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 164
ID ABO31554 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 165
ID ABM07971 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 166
ID ABO40451 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 167
ID ABO35876 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 168
ID ABO44015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 169
ID ADA77922 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 170
ID ABM24810 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 171
ID ABO03078 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US200306131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 172
ID ABR90334 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 173
ID ABM17248 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 174
ID ABR94994 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 175
ID ABR95299 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

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Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 176
ID ADB17095 standard; protein; 720 AA.
DE Human transmembrane PRO polypeptide (SeqID 38).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 177
ID ABO21537 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 178
ID ABR97801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 179
ID ABR87589 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 180
ID ABR77630 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 181
ID ABR27860 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 182
ID ABO06141 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 183
ID ABO03647 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 184
ID ABO35098 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 185
ID ABO26335 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 186
ID ABO48117 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 187
ID ABR92859 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 188
ID ABO24620 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 189
ID ADA37742 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 190
ID ABO11631 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 191
ID ABO02732 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 192
ID ABO16028 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 193
ID ABO27589 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 194
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ID AEM29080 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 195
ID AEM07056 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 196
ID AEM21150 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 197
ID AEM09496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 198
ID ABO41366 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 199
ID ABO36181 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 200
ID ABO43710 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 201
ID AEM76410 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 202
ID AEM76106 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 203
ID AEM25725 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 204
ID AEM26030 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 205
ID ADA21428 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 206
ID ABO03383 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 207
ID ABO02468 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 208
ID ABO44257 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 209
ID ABR90639 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 210
ID ABR73707 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 211
ID ABO16959 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 212
ID ABR94384 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 213
ID ABR75891 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

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PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 214
ID ABR71267 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 215
ID ABR93164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 216
ID ABR93469 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 217
ID ADAL0215 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, PRO1344.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 218
ID ABR87894 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 219
ID ABO27894 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 220
ID ABO30029 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 221
ID ABO3338 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 222
ID ABM04926 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 223
ID ABM08886 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 224
ID ABO36486 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 225
ID ABO35571 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 226
ID ABO39536 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 227
ID ABM10411 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 228
ID ABM1936 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 229
ID ABO52082 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 230
ID ABO52387 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 231
ID ADAL19900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
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Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 232
ID ABO23705 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 233
ID ADB17283 standard; protein; 720 AA.
DE Human transmembrane PRO polypeptide (SeqID 38).
PN US2003050465-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 234
ID ADA17759 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 235
ID ABR97191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054481-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 236
ID ABR86979 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049778-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 237
ID AM11021 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049782-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 238
ID AM28165 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054476-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 239
ID ABO32164 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068733-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 240
ID AM15291 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068692-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 241
ID ABM06446 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068709-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 242
ID ABM04257 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068716-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 243
ID ABM22370 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068740-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 244
ID ABM07666 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068751-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 245
ID ABO40756 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068684-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 246
ID ABM35403 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073179-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 247
ID ABM33166 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 248
ID ABO52692 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049773-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 249
ID ABO50252 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049777-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 250
ID ABU9246 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040055-A1.

Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 270
ID ABO2427 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200305886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 271
ID ABR86369 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 272
ID ABR86674 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 273
ID ABM1638 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 274
ID ABM29690 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 275
ID ABO29114 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 276
ID ABM2895 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 277
ID ABM23285 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 278
ID ABM23065 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 279
ID ABO22147 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054477-A1.
PD 20-MAR-2003.

RESULT 279
ID ABO37706 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 280
ID ABM28470 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 281
ID ABM28775 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 282
ID ABM66419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 283
ID ABM75801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 284
ID ABM34081 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 285
ID ABM34386 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 286
ID ABO20317 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 287
ID ABO21232 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 288
ID ABO22147 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054477-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 289
ID ADA20072 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 290
ID ABO34185 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 291
ID ABR96581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 292
ID ADA94447 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 293
ID ABR85759 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 294
ID ABR99741 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 295
ID ABM00597 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 296
ID ABM00292 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 297
ID ABO29724 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 298
ID ABM23590 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 299
ID ABM29385 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 300
ID ABO38316 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 301
ID ABO45616 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 302
ID ABM20540 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 303
ID ADA81441 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 304
ID ABO16654 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 305
ID ABO18280 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 306
ID ABO22707 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 307
ID ABO23012 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054461-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 308
ID ABR92554 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200306446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 309
ID ABR81511 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 310
ID ABR77935 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 311
ID ABR89724 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 312
ID ABR26640 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 313
ID ABR13766 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 314
ID ABR28504 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 315
ID ABO30334 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 316
ID ABO07361 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

RESULT 317
ID ABO03952 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 318
ID ABO37096 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 319
ID ABO41671 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 320
ID ABO35266 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 321
ID ABR25115 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 322
ID ABO47507 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 323
ID ABO47812 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 324
ID ABO48422 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 325
ID ABO51472 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 326
ID ABO51777 standard; protein; 720 AA.

DE Human PRO polypeptide #85.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 03-APR-2003.
ID ABO50557 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 27-FEB-2003.
ID ABR79681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 27-FEB-2003.
ID ABR16943 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 27-FEB-2003.
ID ABR17975 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 13-FEB-2003.
ID ABO20927 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 13-FEB-2003.
ID ABR96886 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 27-MAR-2003.
ID ADA38672 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein PRO1344.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 27-MAR-2003.
ID ABR12241 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 03-APR-2003.
ID ABR16333 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 03-APR-2003.
ID ABO4636 standard; protein; 720 AA.
DE Human PRO polypeptide #85.

Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 03-APR-2003.
ID ABR24200 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 03-APR-2003.
ID ABR14681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 10-APR-2003.
ID ABR04562 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 10-APR-2003.
ID ABR06751 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 10-APR-2003.
ID ABR09191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 17-APR-2003.
ID ABO39231 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 10-APR-2003.
ID ABR75496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 05-JUN-2003.
ID ABR25420 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 05-JUN-2003.
ID ABR19930 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
PD 05-JUN-2003.
ID ABO4636 standard; protein; 720 AA.
DE Human PRO polypeptide #85.

PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 346
ID ABO47141 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 347
ID ADA83239 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 348
ID ABR71572 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 349
ID ABR72182 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 350
ID ABR98521 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 351
ID ABO06891 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 352
ID ABR84844 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 353
ID ABR73402 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 354
ID ABR76496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 355
ID ABR73097 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 356
ID ABM18163 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 357
ID ABO20622 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 358
ID ABO25365 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 359
ID ABO25670 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 360
ID ABR94079 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 361
ID ADA92793 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 362
ID ABR79986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 363
ID ABM13326 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 364
ID ABO32933 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 365
ID ABR73097 standard; protein; 720 AA.

Best Local Similarity	100.0%;	Pred. No.1.9e-204;
RESULT 365		
ID ABOJ0639 standard; protein; 720 AA.		
DE Human secreted/transmembrane protein (PRO) #85.		
FN US2003064468-A1.		
PD 03-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;
RESULT 366		
ID ABOJ0944 standard; protein; 720 AA.		
DE Human secreted/transmembrane protein (PRO) #85.		
FN US2003064468-A1.		
PD 03-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;
RESULT 367		
ID ABM27250 standard; protein; 720 AA.		
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.		
FN US2003068760-A1.		
PD 10-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;
RESULT 368		
ID ABM29995 standard; protein; 720 AA.		
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.		
FN US2003068769-A1.		
PD 10-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;
RESULT 369		
ID ABM05531 standard; protein; 720 AA.		
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.		
FN US2003045700-A1.		
PD 06-MAR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;
RESULT 370		
ID ABM15596 standard; protein; 720 AA.		
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.		
FN US2003068698-A1.		
PD 10-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;
RESULT 371		
ID ABM06581 standard; protein; 720 AA.		
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.		
FN US2003068759-A1.		
PD 10-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;
RESULT 372		
ID ABO44281 standard; protein; 720 AA.		
DE Human secreted/transmembrane protein (PRO) #85.		
FN US2003049748-A1.		
PD 13-MAR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;
RESULT 373		
ID ABO38011 standard; protein; 720 AA.		
DE Human secreted/transmembrane protein (PRO) #85.		
FN US2003068765-A1.		
PD 10-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;
RESULT 374		
ID ABO38011 standard; protein; 720 AA.		
DE Human secreted/transmembrane protein (PRO) #85.		
FN US2003068765-A1.		
PD 10-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 6; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.9e-204;

RESULT 374	ID	ABO45921 standard; protein; 720 AA.			
	DE	Human PRO polypeptide #85.			
	PN	US2003049754-A1.			
	PD	13-MAR-2003.			
	PA	(GETH) GENENTECH INC.			
	Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 375	ID	ABM6724 standard; protein; 720 AA.			
	DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.			
	PN	US2003068688-A1.			
	PD	10-APR-2003.			
	PA	(GETH) GENENTECH INC.			
	Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 376	ID	ADH20282 standard; protein; 720 AA.			
	DE	Human secreted/transmembrane protein (PRO) #85.			
	PN	US2003082767-A1.			
	PD	01-MAY-2003.			
	Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 377	ID	ABM19625 standard; protein; 720 AA.			
	DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.			
	PN	US2003104552-A1.			
	PD	05-JUN-2003.			
	PA	(GETH) GENENTECH INC.			
	Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 378	ID	ABO49337 standard; protein; 720 AA.			
	DE	Human secreted/transmembrane protein (PRO) #85.			
	PN	US2003049774-A1.			
	PD	13-MAR-2003.			
	PA	(GETH) GENENTECH INC.			
	Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 379	ID	ABO49642 standard; protein; 720 AA.			
	DE	Human secreted/transmembrane protein (PRO) #85.			
	PN	US2003049775-A1.			
	PD	13-MAR-2003.			
	PA	(GETH) GENENTECH INC.			
	Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 380	ID	ADA78534 standard; protein; 720 AA.			
	DE	Human secreted/transmembrane protein (PRO) #85.			
	PN	US2003073181-A1.			
	PD	17-APR-2003.			
	PA	(GETH) GENENTECH INC.			
	Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 381	ID	ABR88199 standard; protein; 720 AA.			
	DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.			
	PN	US2003068720-A1.			
	PD	10-APR-2003.			
	PA	(GETH) GENENTECH INC.			
	Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 382	ID	ADA00369 standard; protein; 720 AA.			
	DE	Human secreted/transmembrane polypeptide PRO 1344.			
	PN	US2003027992-A1.			
	PD	06-FEB-2003.			
	PA	(GETH) GENENTECH INC.			
	Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 1.9e-204;		
RESULT 383	ID	ABM26945 standard; protein; 720 AA.			

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID AM03342 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABO39841 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABO49947 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABO50862 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003048780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABO05318 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR74622 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR77101 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABM17858 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR95909 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABO21842 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABO20012 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABO24315 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR86064 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABM10716 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABM76715 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR89419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABM12546 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABM05836 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABO34961 standard; protein; 720 AA.
DE Human PRO polypeptide #85.

PN US2003068728-A1.
RESULT 403
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR03037 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR19015 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR19320 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR046531 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR049032 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR69075 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR89114 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR72487 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR74317 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR019585 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR80291 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR01512 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR01512 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR87284 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR12851 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR30605 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR24505 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR029419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR029419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR029419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
ID ABR029419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 441
ID ABM14071 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 442
ID ABM08276 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 443
ID ABO040146 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 444
ID ABM74581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 445
ID ABM33776 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 446
ID ABM20235 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 447
ID ABO48727 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 448
ID ABO22540 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 449
ID ABR72792 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 450
ID ABO15434 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 451
ID ABR85149 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 452
ID ABO15129 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 453
ID ABO17264 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 454
ID ABM17553 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 455
ID ABO06520 standard; protein; 720 AA.
DE Human secreted/transmembrane PRO polypeptide #65.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 456
ID AOB39213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 457
ID ABR85454 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 458
ID ABM77020 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 459
ID ABO28199 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
ID	ABM3471 standard; protein; 720 AA.	
RESULT 469	DE Human secreted polypeptide PRO1344, SEQ ID NO:170.	
PN	US2003096357-A1.	
PD	22-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 470	ID ABO46226 standard; protein; 720 AA.	
ID	Human PRO polypeptide #85.	
PN	US2003049760-A1.	
PD	13-MAR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 471	ID ADA82605 standard; protein; 720 AA.	
DE	Human secreted/transmembrane protein (PRO) #85.	
PN	US2003049755-A1.	
PD	13-MAR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 472	ID ADB85611 standard; protein; 720 AA.	
DE	Novel human secreted and transmembrane protein PRO1344.	
PN	US2003049735-A1.	
PD	13-MAR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 473	ID ADB96239 standard; protein; 720 AA.	
DE	Human PRO polypeptide #65.	
PN	US2003054403-A1.	
PD	20-MAR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 474	ID ABBM31825 standard; protein; 720 AA.	
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.	
PN	US2003068680-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 475	ID ABBM31215 standard; protein; 720 AA.	
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.	
PN	US1003068762-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 476	ID ADB85913 standard; protein; 720 AA.	
DE	Human secreted/transmembrane protein (PRO) #85.	
PN	US2003054472-A1.	
PD	20-MAR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 477	ID ABBM32130 standard; protein; 720 AA.	
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.	
PN	US2003068708-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.9e-204;
RESULT 478	ID ABBM32435 standard; protein; 720 AA.	

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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 498
ID ADC82421 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 499
ID ADD05643 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 500
ID ADD08601 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 501
ID ADD06850 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 502
ID ADC83097 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 503
ID ADD55204 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 504
ID ADD36042 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 505
ID ADD56162 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 506
ID ADD54600 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 507
ID ADE26754 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.

PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 508
ID ADE26221 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 509
ID ADF67158 standard; protein; 720 AA.
DE Human PRO1344 amino acid sequence SEQ ID NO:231.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 510
ID ADG01043 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 511
ID ADG08596 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 512
ID ADG02638 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 513
ID ADG01345 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 514
ID ADF95520 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 515
ID ADF95217 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 516
ID ADG12335 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 517
ID ADH24070 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 518
ID ADH34096 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 519
ID ADH29929 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 520
ID ADH23900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 521
ID ADH08995 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 522
ID ADG85304 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 523
ID ADH24580 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 524
ID ADH37436 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 525
ID ADH02025 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

RESULT 526
ID ADH37606 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 527
ID ADG85644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 528
ID ADH24240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 529
ID ADH38534 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 530
ID ADG83655 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 531
ID ADH29463 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 532
ID ADH27579 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 533
ID ADH37776 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 534
ID ADH37953 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 535

ID ADH57373 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 536
ID ADH53515 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 537
ID ADH53685 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 538
ID ADH52021 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 539
ID ADH49676 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 540
ID ADI25386 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 541
ID ADH90179 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 542
ID ADI25556 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 543
ID ADH97730 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 544
ID ADI35412 standard; protein; 720 AA.

DE Human PRO polypeptide #65.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 545
ID ADI03578 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 546
ID ADI11935 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 547
ID ADH90009 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 548
ID ADH99904 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 549
ID ADH99410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 550
ID ADI11085 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 551
ID ADI11595 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 552
ID ADH96240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 553
ID ADH96580 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181708-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 554
ID ADH98070 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 555
ID ADI05058 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 556
ID ADI03408 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 557
ID ADI04603 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 558
ID ADH78257 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 559
ID ADI19601 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 560
ID ADH90349 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 561
ID ADI03068 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 562
ID ADH77917 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 563
ID ADH97900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 564
ID ADI01285 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 565
ID ADI01980 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 566
ID ADI03238 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 567
ID ADI11425 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 568
ID ADI02327 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 569
ID ADI11765 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 570
ID ADI05402 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 571
ID ADH79474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 572
ID ADH79474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 572
ID ADI19431 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 573
ID ADI05232 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 574
ID ADH79644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 575
ID ADI01470 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 576
ID ADI01640 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 577
ID ADI01810 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 578
ID ADH79814 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 579
ID ADI04632 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 580
ID ADI02768 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

RESULT 581
ID ADH78087 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 582
ID ADI25726 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 583
ID ADI25896 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 584
ID ADK65408 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 585
ID ADH98750 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 586
ID ADH79991 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 587
ID ADL32776 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 588
ID ADM30310 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 589
ID ADL37722 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 590

ID ADC52176 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 591
ID ADE74307 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 592
ID ADE74919 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003211574-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 593
ID ADP35357 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 594
ID ADG11607 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003226655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 595
ID ADP96132 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215909-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 596
ID ADG04403 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 597
ID ADG050563 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 598
ID ADH06608 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 599
ID ADH06438 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 600
ID ADG68659 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 601
ID ADH27749 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 602
ID ADH25090 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 603
ID ADH33722 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 604
ID ADG82819 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 605
ID ADH02365 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 606
ID ADH07972 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 607
ID ADG69369 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 608
ID ADH39190 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 609
ID ADH26100 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 610
ID ADG83930 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 611
ID ADH19477 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 612
ID ADG85474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003168848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 613
ID ADH05268 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 614
ID ADH30098 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 615
ID ADH24410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 616
ID ADH33069 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 617
ID ADG69539 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

RESULT 618
ID ADH07802 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 619
ID ADG85814 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 620
ID ADH33360 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 621
ID ADH33552 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 622
ID ADH33892 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 623
ID ADH01102 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 624
ID ADG69709 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 625
ID ADH20970 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 626
ID ADH02195 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 627
ID ADG69199 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 628
ID ADG85984 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 629
ID ADH24920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 630
ID ADH39537 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 631
ID ADH20010 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 632
ID ADH02535 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 633
ID ADG69029 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 634
ID ADH07632 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 635
ID ADG86154 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 636
ID ADH24750 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 637
ID ADH25798 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 638
ID ADH38364 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 639
ID ADH57203 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 640
ID ADH52191 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 641
ID ADH49557 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 642
ID ADH90519 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 643
ID ADI11255 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 644
ID ADH98920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 645
ID ADI02150 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190699-A1.

PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 646
ID ADH90689 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 647
ID ADJ54808 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 648
ID ADJ98564 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 649
ID ADJ98734 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 650
ID ADH78893 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 651
ID ADJ99127 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 652
ID ADJ99297 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 653
ID ADJ99815 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 654
ID ADH79063 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 655
ID ADK00923 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 656
ID ADK1444 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 657
ID ADJ64579 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 658
ID ADM31475 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 659
ID ADM36522 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 660
ID ADM40327 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 661
ID ADM80893 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 662
ID ADN37935 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 663
ID ADY77733 standard; protein; 720 AA.
DE Neoplastic disease detection protein PRO1344.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.

PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A. J.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 3945; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 664
ID AEA38494 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #133.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 665
ID AED50165 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2005163766-A1.
PD 28-JUL-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 3945; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 666
ID AEF12564 standard; protein; 720 AA.
DE Human PRO1344 protein SEQ ID NO:38.
PN US200608901-A1.
PD 12-JAN-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 667
ID AEF74253 standard; protein; 720 AA.
DE Human PRO1344 protein SEQ ID NO:38.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 3945; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 668
ID AEG62857 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2006073544-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 669
ID AEG72680 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2006074226-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 670
ID AEG62245 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2006073545-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
Query Match 100.0%; Score 3945; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;

RESULT 671
ID AEG88162 standard; protein; 720 AA.
DE Human PRO protein amino acid sequence - SEQ ID 170.
PN US2006074227-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 672
ID AEF17478 standard; protein; 720 AA.
DE Human tumor overexpressed cDNA protein product PRO1344 SEQ ID NO: 170.
PN US2006094864-A1.
PD 04-MAY-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 673
ID AEA43591 standard; protein; 720 AA.
DE PRO1344 protein sequence, SEQ ID 38.
PN US200609657-A1.
PD 11-MAY-2006.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 3945; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 674
ID AEF11916 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2006160186-A1.
PD 20-JUL-2006.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 3945; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
RESULT 675
ID AAB70532 standard; protein; 720 AA.
DE Human PRO2 protein sequence SEQ ID NO:4.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 99.8%; Score 3939; DB 4; Length 720;
Best Local Similarity 99.7%; Pred. No. 4e-204;
RESULT 676
ID AAU0401 standard; protein; 720 AA.
DE Human secreted protein, POLY13.
PN WO200119856-A2.
PD 22-MAR-2001.
PA (CURA-) CURAGEN CORP.
Query Match 99.8%; Score 3939; DB 4; Length 720;
Best Local Similarity 99.7%; Pred. No. 4e-204;
RESULT 677
ID ADH89028 standard; protein; 720 AA.
DE Human POLYX polypeptide #13.
PN US2003198958-A1.
PD 23-OCT-2003.
PA (SHIW/) SHIMKETS R A.
PA (FERN/) FERNANDES E.
PA (HERR/) HERRMANN J L.
PA (LITX/) LIU X.

PA (YANG/) YANG M.
PA (BOLD/) BOLDOG F L.
PA (SMIT/) BOLDOGSON G.
PA (RAST/) RASTBELI L.
Query Match 99.8%; Score 3939; DB 8; Length 720;
RESULT 678
ID AAY88280 standard; protein; 720 AA.
DE Human TANGO 215 protein.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 99.8%; Score 3936; DB 3; Length 720;
RESULT 679
ID AE16805 standard; protein; 720 AA.
DE Human TANGO 215 protein.
PN US2006141575-A1.
PD 29-JUN-2006.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 99.8%; Score 3936; DB 10; Length 720;
RESULT 680
ID ADY80612 standard; protein; 737 AA.
DE Human regeneration-associated muscle protease enzyme - SEQ ID 2.
PN JP2005073574-A.
PD 24-MAR-2005.
PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
Query Match 99.5%; Score 3926.5; DB 9; Length 737;
RESULT 681
ID AAB85891 standard; protein; 737 AA.
DE Human serine protease-like protein (hc-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 737;
RESULT 682
ID AAB93670 standard; protein; 737 AA.
DE Human protein sequence SEQ ID NO:13202.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 737;
RESULT 683
ID ADJ69990 standard; protein; 737 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1796.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 99.4%; Score 3921.5; DB 7; Length 737;
RESULT 684
ID ADN04640 standard; protein; 737 AA.
DE Antipsoriatic protein sequence #505.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
RESULT 685
ID ADS85034 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SeqID36.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
RESULT 686
ID (UTJU-) UNIV JUNTENDO.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
RESULT 686
Best Local Similarity 97.6%; Pred. No. 3.6e-203;

ID ADS85022 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SeqID24.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
RESULT 687
ID AAB85893 standard; protein; 762 AA.
DE Human serine protease-like protein (hc-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 762;
RESULT 688
ID AE168109 standard; protein; 699 AA.
DE Human TANGO 215 mature protein SEQ ID NO: 86.
PN US2006141575-A1.
PD 29-JUN-2006.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 97.0%; Score 3828; DB 10; Length 699;
RESULT 689
ID ADY80614 standard; protein; 720 AA.
DE Mouse regeneration-associated muscle protease enzyme - SEQ ID 4.
PN JP2005073574-A.
PD 24-MAR-2005.
PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
Query Match 91.7%; Score 3617; DB 9; Length 720;
RESULT 690
ID AE168141 standard; protein; 720 AA.
DE Murine TANGO 215 protein SEQ ID NO: 118.
PN US2006141575-A1.
PD 29-JUN-2006.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 91.7%; Score 3617; DB 10; Length 720;
RESULT 691
ID AAB85892 standard; protein; 720 AA.
DE Mouse serine protease-like protein (mc-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 91.6%; Score 3612; DB 4; Length 720;
RESULT 692
ID AAB09927 standard; protein; 719 AA.
DE Murine TANGO 215 protein.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 91.3%; Score 3602.5; DB 3; Length 719;
RESULT 693
ID AE168169 standard; protein; 720 AA.
DE Murine TANGO 215 protein.
PN US2006141575-A1.
PD 29-JUN-2006.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 91.0%; Score 3591; DB 10; Length 720;
RESULT 694
ID AAB19180 standard; protein; 649 AA.
DE Human protease, PRS-17 protein.
PN WO200208396-A2.
PD 31-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 88.7%; Score 3500.5; DB 5; Length 649;
RESULT 695
Best Local Similarity 90.0%; Pred. No. 1.5e-180;

ID AAB70531 standard; protein; 567 AA.
DE Human PRO1 protein sequence SEQ ID NO:2.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 78.3%; Score 3089.5; DB 4; Length 567;
Best Local Similarity 99.5%; Pred. No. 1.9e-158;
RESULT 696
ID AAB49533 standard; protein; 570 AA.
DE Clone HEPPEY75.
PN WO200061774-A2.
PD 13-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.7%; Score 2946.5; DB 3; Length 570;
Best Local Similarity 96.8%; Pred. No. 9.4e-151;
RESULT 697
ID ADR41465 standard; protein; 551 AA.
DE Human CD-like molecule HSXDF41, SEQ ID NO:284.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.6%; Score 2944; DB 5; Length 551;
Best Local Similarity 99.3%; Pred. No. 1.2e-150;
RESULT 698
ID AAM41706 standard; protein; 499 AA.
DE Human polypeptide SEQ ID NO 6637.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 65.3%; Score 2577.5; DB 4; Length 499;
Best Local Similarity 96.6%; Pred. No. 6.2e-131;
RESULT 699
ID AAE20617 standard; protein; 455 AA.
DE Human gene 5 encoded secreted protein HSLGU75, SEQ ID NO:79.
PN WO200118435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 61.2%; Score 2413; DB 5; Length 455;
Best Local Similarity 99.3%; Pred. No. 4.2e-122;
RESULT 700
ID ABG64652 standard; protein; 455 AA.
DE Human albumin fusion protein #1327.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 61.2%; Score 2413; DB 5; Length 455;
Best Local Similarity 99.3%; Pred. No. 4.2e-122;
RESULT 701
ID ADL77919 standard; protein; 455 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1401.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 61.2%; Score 2413; DB 8; Length 455;
Best Local Similarity 99.3%; Pred. No. 4.2e-122;
RESULT 702
ID AEH08193 standard; protein; 455 AA.
DE Therapeutic protein HSLGU75, SEQ ID 1401.
PN US2006084794-A1.
PD 20-APR-2006.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 61.2%; Score 2413; DB 10; Length 455;
Best Local Similarity 99.3%; Pred. No. 4.2e-122;
RESULT 703
ID ADL06662 standard; protein; 417 AA.
DE Human 3T3 cell conversion promoter PP938.
PN CN1403477-A.
PD 19-MAR-2003.
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
Query Match 52.2%; Score 2059; DB 7; Length 417;
Best Local Similarity 95.6%; Pred. No. 4.5e-103;
RESULT 704

ID AAM39920 standard; protein; 359 AA.
DE Human polypeptide SEQ ID NO 3065.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 48.4%; Score 1909; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.7e-95;
RESULT 705
ID AAM39957 standard; protein; 359 AA.
DE Human polypeptide SEQ ID NO 3102.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 48.4%; Score 1909; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.7e-95;
RESULT 706
ID AAE20797 standard; protein; 323 AA.
DE Human gene 5 encoded secreted protein HSLGU75, SEQ ID NO:59.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 43.3%; Score 1708.5; DB 5; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.7e-84;
RESULT 707
ID ABG64653 standard; protein; 323 AA.
DE Human albumin fusion protein #1328.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 43.3%; Score 1708.5; DB 5; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.7e-84;
RESULT 708
ID ADL77920 standard; protein; 323 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1402.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 43.3%; Score 1708.5; DB 8; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.7e-84;
RESULT 709
ID AEH08194 standard; protein; 323 AA.
DE Therapeutic protein HSLGU75, SEQ ID 1402.
PN US2006084794-A1.
PD 20-APR-2006.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 43.3%; Score 1708.5; DB 10; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.7e-84;
RESULT 710
ID AAM24485 standard; protein; 234 AA.
DE Human EST encoded protein SEQ ID NO: 2010.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 29.8%; Score 1175.5; DB 4; Length 234;
Best Local Similarity 91.4%; Pred. No. 1e-55;
RESULT 711
ID ABR72332 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN WO200302976-A2.
PD 09-JAN-2003.
PA (WHIK-) BIONEER INC.
Query Match 17.0%; Score 672; DB 6; Length 1019;
Best Local Similarity 25.6%; Pred. No. 5.3e-28;
RESULT 712
ID AAM43394 standard; protein; 1019 AA.
DE Singapore horseshoe crab factor C proenzyme (CrFC 21).
PN SG42456-A1.
PD 15-AUG-1997.
PA (UTST-) UNITV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 713

ID AAY05750 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN W09915676-A1.
PD 01-APR-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 714
ID AAM94302 standard; protein; 1019 AA.
DE Horseshoe crab Factor C protein #2.
PN US5858706-A.
PD 12-JAN-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 715
ID AAY42490 standard; protein; 1019 AA.
DE Recombinant N-terminally truncated Horseshoe crab Factor C protein.
PN US5985590-A.
PD 16-NOV-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 3; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 716
ID AAB60935 standard; protein; 1019 AA.
DE Horseshoe crab recombinant Factor C #2.
PN W0200127289-A2.
PD 19-APR-2001.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 4; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 717
ID ABP72334 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN W02003002976-A2.
PD 09-JAN-2003.
PA (WHIK) BICWHITTAKER INC.
Query Match 16.9%; Score 665; DB 6; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 718
ID ADM39099 standard; protein; 1019 AA.
DE Southeast Asian horseshoe crab Factor C.
PN W02005003163-A1.
PD 13-JAN-2005.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 9; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 719
ID AAM43393 standard; protein; 1083 AA.
DE Singapore horseshoe crab Factor C proenzyme (CrFC 26).
PN S642456-A1.
PD 15-AUG-1997.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 720
ID AAY05749 standard; protein; 1083 AA.
DE Horseshoe crab Factor C.
PN W09915676-A1.
PD 01-APR-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 721
ID AAM94301 standard; protein; 1083 AA.
DE Horseshoe crab Factor C protein #1.
PN US5858706-A.
PD 12-JAN-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 722
ID AAY42489 standard; protein; 1083 AA.

DE Horseshoe crab recombinant Factor C protein.
PN US5985590-A.
PD 16-NOV-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 3; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 723
ID AAB60934 standard; protein; 1083 AA.
DE Horseshoe crab recombinant Factor C #1.
PN W0200127289-A2.
PD 19-APR-2001.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 4; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 724
ID ABP72333 standard; protein; 1083 AA.
DE Horseshoe crab Factor C.
PN W02003002976-A2.
PD 09-JAN-2003.
PA (WHIK) BICWHITTAKER INC.
Query Match 16.9%; Score 665; DB 6; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.3e-27;
RESULT 725
ID AAM41743 standard; protein; 146 AA.
DE Human polypeptide SEQ ID NO 6674.
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 16.8%; Score 662; DB 4; Length 146;
Best Local Similarity 85.4%; Pred. No. 3e-28;
RESULT 726
ID AAY11743 standard; protein; 103 AA.
DE Human 5' EST secreted protein SEQ ID NO: 343.
PN W09906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 14.7%; Score 580; DB 2; Length 103;
Best Local Similarity 97.1%; Pred. No. 5.6e-24;
RESULT 727
ID AEF13693 standard; protein; 699 AA.
DE Human MBP-associated serine protease 1 (MASP-1) protein.
PN W02005123776-A1.
PD 28-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 12.1%; Score 478; DB 10; Length 699;
Best Local Similarity 24.6%; Pred. No. 1.1e-17;
RESULT 728
ID AEB26839 standard; protein; 680 AA.
DE Human MASP-1 protein, SEQ ID NO: 6 #2.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSEN J C.
Query Match 12.1%; Score 476; DB 9; Length 680;
Best Local Similarity 24.6%; Pred. No. 1.3e-17;
RESULT 729
ID ADE87459 standard; protein; 699 AA.
DE Human MBP-associated serine protease-1 protein.
PN EP1344533-A1.
PD 17-SEP-2003.
PA (NATL-) NATLMONE AS.
Query Match 12.1%; Score 476; DB 7; Length 699;
Best Local Similarity 24.6%; Pred. No. 1.3e-17;
RESULT 730
ID AEB64931 standard; protein; 699 AA.
DE Human p100 serine protease of Ra-reactive factor, SEQ ID 24.
PN UP2005253434-A.
PD 22-SEP-2005.
PA (HOKK-) HOKKAIDO TLO KK.
Query Match 12.1%; Score 476; DB 10; Length 699;
Best Local Similarity 24.6%; Pred. No. 1.3e-17;
RESULT 731

ID ADL91028 standard; protein; 699 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:14.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATL-) NATIMMUNE AS.
Query Match 12.0%; Score 475; DB 8; Length 699;
Best Local Similarity 24.6%; Pred. No. 1.5e-17;
RESULT 732
ID AM83722 standard; protein; 698 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3971.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.0%; Score 474.5; DB 8; Length 698;
Best Local Similarity 24.4%; Pred. No. 1.6e-17;
RESULT 733
ID AAB85060 standard; protein; 728 AA.
DE Human serine protease MASP-3 polypeptide.
PN WO200140451-A2.
PD 07-JUN-2001.
PA (JENS/) JENSENIUS J C.
Query Match 11.9%; Score 471; DB 4; Length 728;
Best Local Similarity 25.0%; Pred. No. 2.6e-17;
RESULT 734
ID AEB26835 standard; protein; 679 AA.
DE Human MASP-1 protein, SEQ ID NO: 6 #1.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
Query Match 11.9%; Score 469.5; DB 9; Length 679;
Best Local Similarity 24.4%; Pred. No. 2.9e-17;
RESULT 735
ID ADE87461 standard; protein; 728 AA.
DE Human MBL-associated serine protease-4 protein.
PN EP134453-A1.
PD 17-SEP-2003.
PA (NATL-) NATIMMUNE AS.
Query Match 11.9%; Score 468; DB 7; Length 728;
Best Local Similarity 25.0%; Pred. No. 3.8e-17;
RESULT 736
ID ADJ1027 standard; protein; 728 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:13.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATL-) NATIMMUNE AS.
Query Match 11.9%; Score 468; DB 8; Length 728;
Best Local Similarity 25.0%; Pred. No. 3.8e-17;
RESULT 737
ID AAB47559 standard; protein; 728 AA.
DE Protease PRS-1.
PN WO200171004-A2.
PD 27-SEP-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.7%; Score 461; DB 4; Length 728;
Best Local Similarity 24.9%; Pred. No. 9e-17;
RESULT 738
ID AAG80756 standard; protein; 707 AA.
DE Murine C1r protein.
PN KR2001077614-A.
PD 20-AUG-2001.
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.
Query Match 10.9%; Score 429; DB 5; Length 707;
Best Local Similarity 22.3%; Pred. No. 4.6e-15;
RESULT 739
ID AEF03476 standard; protein; 670 AA.
DE Mature rat MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 10.4%; Score 412; DB 10; Length 670;
Best Local Similarity 21.4%; Pred. No. 3.6e-14;
RESULT 740
ID AEF03475 standard; protein; 685 AA.
DE Full length rat MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 10.7%; Score 423; DB 10; Length 685;
Best Local Similarity 24.1%; Pred. No. 9.5e-15;
RESULT 741
ID AEF03473 standard; protein; 670 AA.
DE Mature murine MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 10.4%; Score 412; DB 10; Length 670;
Best Local Similarity 21.4%; Pred. No. 3.6e-14;
RESULT 742
ID AEF03472 standard; protein; 685 AA.
DE Full length murine MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 10.4%; Score 412; DB 10; Length 685;
Best Local Similarity 21.4%; Pred. No. 3.7e-14;
RESULT 743
ID AEB26836 standard; protein; 688 AA.
DE Human C1q-associated serine protease, C1r SEQ ID NO: 7.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
Query Match 10.2%; Score 403.5; DB 9; Length 688;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 744
ID ABB50288 standard; protein; 705 AA.
DE Complement component 1 r ovarian tumour marker protein, SEQ ID NO:66.
PN WO2001751177-A2.
PD 11-OCT-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 10.2%; Score 403.5; DB 4; Length 705;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 745
ID AAG80757 standard; protein; 705 AA.
DE Human C1r protein.
PN KR2001077614-A.
PD 20-AUG-2001.
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.
Query Match 10.2%; Score 403.5; DB 5; Length 705;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 746
ID ADP65211 standard; protein; 705 AA.
DE Human complement component 1, r subcomponent.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 10.2%; Score 403.5; DB 7; Length 705;
Best Local Similarity 22.6%; Pred. No. 1.1e-13;
RESULT 747
ID AEB13349 standard; protein; 705 AA.
DE Complement component C1r SEQ ID NO 14.
PN WO2005061537-A2.
PD 07-JUL-2005.
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
Query Match 10.2%; Score 403.5; DB 9; Length 705;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 748

Query Match 10.7%; Score 423; DB 10; Length 670;
Best Local Similarity 24.1%; Pred. No. 9.3e-15;
RESULT 740
ID AEF03475 standard; protein; 685 AA.
DE Full length rat MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 10.7%; Score 423; DB 10; Length 685;
Best Local Similarity 24.1%; Pred. No. 9.5e-15;
RESULT 741
ID AEF03473 standard; protein; 670 AA.
DE Mature murine MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 10.4%; Score 412; DB 10; Length 670;
Best Local Similarity 21.4%; Pred. No. 3.6e-14;
RESULT 742
ID AEF03472 standard; protein; 685 AA.
DE Full length murine MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 10.4%; Score 412; DB 10; Length 685;
Best Local Similarity 21.4%; Pred. No. 3.7e-14;
RESULT 743
ID AEB26836 standard; protein; 688 AA.
DE Human C1q-associated serine protease, C1r SEQ ID NO: 7.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
Query Match 10.2%; Score 403.5; DB 9; Length 688;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 744
ID ABB50288 standard; protein; 705 AA.
DE Complement component 1 r ovarian tumour marker protein, SEQ ID NO:66.
PN WO2001751177-A2.
PD 11-OCT-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 10.2%; Score 403.5; DB 4; Length 705;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 745
ID AAG80757 standard; protein; 705 AA.
DE Human C1r protein.
PN KR2001077614-A.
PD 20-AUG-2001.
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.
Query Match 10.2%; Score 403.5; DB 5; Length 705;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 746
ID ADP65211 standard; protein; 705 AA.
DE Human complement component 1, r subcomponent.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 10.2%; Score 403.5; DB 7; Length 705;
Best Local Similarity 22.6%; Pred. No. 1.1e-13;
RESULT 747
ID AEB13349 standard; protein; 705 AA.
DE Complement component C1r SEQ ID NO 14.
PN WO2005061537-A2.
PD 07-JUL-2005.
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
Query Match 10.2%; Score 403.5; DB 9; Length 705;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 748

ID AED74704 standard; protein; 705 AA.
DE Human placental protein SEQ ID NO:1532.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 10.2%; Score 403.5; DB 9; Length 705;
Best Local Similarity 22.9%; Pred. No. 1.1e-13;
RESULT 749
ID ADU18123 standard; protein; 704 AA.
DE Human candidate osteoarthritis marker protein - SEQ ID 154.
PN WO2004092413-A2.
PD 28-OCT-2004.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match 10.2%; Score 403; DB 8; Length 704;
Best Local Similarity 22.5%; Pred. No. 1.2e-13;
RESULT 750
ID AEG31619 standard; protein; 686 AA.
DE Human mannan-binding lectin associated serine protease-2 protein.
PN US2002082208-A1.
PD 27-JUN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 751
ID AAE14564 standard; protein; 686 AA.
DE Human MASP-2 protein.
PN WO200206460-A2.
PD 24-JAN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 752
ID AEG32115 standard; protein; 686 AA.
DE Mannan-binding lectin associated serine protease-2 (MASP-2).
PN US2002082209-A1.
PD 27-JUN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 753
ID ADL91025 standard; protein; 686 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:11.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATI-) NATIMUNE AS.
Query Match 10.2%; Score 401.5; DB 8; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 754
ID AEA17053 standard; protein; 686 AA.
DE Alzheimer's disease associated protein #6.
PN US2005123962-A1.
PD 09-JUN-2005.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 10.2%; Score 401.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 755
ID AEB26831 standard; protein; 686 AA.
DE Human mannan binding lectin-associated serine protease-2, SEQ ID NO: 2.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 756
ID AEF03426 standard; protein; 686 AA.
DE Full length MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.

PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.2%; Score 401.5; DB 10; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 757
ID AEF13655 standard; protein; 686 AA.
DE Human MB1-associated serine protease 2 (MASP-2) protein.
PN WO2005123776-A1.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.2%; Score 401.5; DB 10; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 758
ID AAE14568 standard; protein; 686 AA.
DE Human MASP-2 protein, alternative version.
PN WO200206460-A2.
PD 24-JAN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 400.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.5e-13;
RESULT 759
ID ADE87460 standard; protein; 686 AA.
DE Human MB1-associated serine protease-2 protein.
PN EPI34453-A1.
PD 17-SEP-2003.
PA (NATI-) NATIMUNE AS.
Query Match 10.2%; Score 400.5; DB 7; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.5e-13;
RESULT 760
ID ADV50598 standard; protein; 686 AA.
DE Human mannan-binding lectin serine protease 2 (MASP2) protein.
PN WO2004106384-A1.
PD 09-DEC-2004.
PA (NATI-) NATIMUNE AS.
Query Match 10.2%; Score 400.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.5e-13;
RESULT 761
ID ADY62954 standard; protein; 686 AA.
DE human mitogen activated serine protease-2 (MASP-2).
PN WO2005024013-A1.
PD 17-MAR-2005.
PA (NATI-) NATIMUNE AS.
Query Match 10.2%; Score 400.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.5e-13;
RESULT 762
ID ADQ27010 standard; protein; 671 AA.
DE Human MASP-2 mature polypeptide.
PN WO2004050907-A2.
PD 17-JUN-2004.
PA (UYAA-) UNIV AARHUS.
PA (AARH) AARHUS AMT.
Query Match 10.1%; Score 399.5; DB 8; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.7e-13;
RESULT 763
ID AEB26838 standard; protein; 671 AA.
DE Human mature MASP-2 protein (residues 16-686).
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.1%; Score 399.5; DB 9; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.7e-13;
RESULT 764
ID AEF03427 standard; protein; 671 AA.
DE Mature MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.1%; Score 399.5; DB 10; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.7e-13;

RESULT 765
ID AEF13656 standard; protein; 671 AA.
DE Human MBL-associated serine protease 2 (MASP-2) mature protein.
PN W02005123776-A1.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match
Best Local Similarity 10.1%; Score 399.5; DB 10; Length 671;
PRED. NO. 1.7e-13;
RESULT 766
ID AAE14565 standard; peptide; 671 AA.
DE Human mature MASP-2 protein.
PN W0200206460-A2.
PD 24-JAN-2002.
PA (JENS/) JENSENIUS J C.
Query Match
Best Local Similarity 10.1%; Score 398.5; DB 5; Length 671;
PRED. NO. 1.9e-13;
RESULT 767
ID AEC95282 standard; protein; 604 AA.
DE Enteropeptidase, SEQ ID 5.
PN JP2005253325-A.
PD 22-SEP-2005.
PA (UYHO-) UNIV HOKKAIDO.
Query Match
Best Local Similarity 9.4%; Score 369.5; DB 9; Length 604;
PRED. NO. 6.4e-12;
RESULT 768
ID AEC95280 standard; protein; 1036 AA.
DE Enteropeptidase, SEQ ID 3.
PN JP2005253325-A.
PD 22-SEP-2005.
PA (UYHO-) UNIV HOKKAIDO.
Query Match
Best Local Similarity 9.4%; Score 369.5; DB 9; Length 1036;
PRED. NO. 1.1e-11;
RESULT 769
ID ADX26355 standard; protein; 694 AA.
DE Novel cell pain response detection method-related mouse protein SeqID701.
PN W02005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match
Best Local Similarity 9.2%; Score 364; DB 9; Length 694;
PRED. NO. 1.4e-11;
RESULT 770
ID ADE56422 standard; protein; 694 AA.
DE Rat Protein BAA25797, SEQ ID NO 11123.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match
Best Local Similarity 8.6%; Score 340.5; DB 7; Length 694;
PRED. NO. 2.7e-10;
RESULT 771
ID ADE83526 standard; protein; 694 AA.
DE Rat Protein BAA25797, SEQ ID NO 11123.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match
Best Local Similarity 8.6%; Score 340.5; DB 7; Length 694;
PRED. NO. 2.7e-10;
RESULT 772
ID ADX26430 standard; protein; 694 AA.
DE Novel cell pain response detection method-related rat protein SeqID776.
PN W02005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match
Best Local Similarity 8.6%; Score 340.5; DB 9; Length 694;
PRED. NO. 2.7e-10;
RESULT 773
ID ADE56418 standard; protein; 695 AA.
DE Rat Protein DB8250, SEQ ID NO 2271.
PN W02003016475-A2.
PD 27-FEB-2003.

PA (GEHO) GEN HOSPITAL CORP.
Query Match
Best Local Similarity 8.6%; Score 340.5; DB 7; Length 695;
PRED. NO. 2.7e-10;
RESULT 774
ID ADD4538 standard; protein; 695 AA.
DE Rat Protein DB8250, SEQ ID NO 10771.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match
Best Local Similarity 8.6%; Score 340.5; DB 7; Length 695;
PRED. NO. 2.7e-10;
RESULT 775
ID AAB43579 standard; protein; 760 AA.
DE Human cancer associated protein sequence SEQ ID NO:1024.
PN W020053530-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 8.5%; Score 336; DB 3; Length 760;
PRED. NO. 5.1e-10;
RESULT 776
ID AEB26837 standard; protein; 673 AA.
DE Human C1q-associated serine protease, C1s SEQ ID NO: 8.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
Query Match
Best Local Similarity 8.5%; Score 334; DB 9; Length 673;
PRED. NO. 5.8e-10;
RESULT 777
ID ADD45340 standard; protein; 688 AA.
DE Human Protein O9UCV3, SEQ ID NO 10773.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match
Best Local Similarity 8.5%; Score 334; DB 7; Length 688;
PRED. NO. 5.9e-10;
RESULT 778
ID ADE56420 standard; protein; 688 AA.
DE Human Protein O9UCV3, SEQ ID NO 2273.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match
Best Local Similarity 8.5%; Score 334; DB 7; Length 688;
PRED. NO. 5.9e-10;
RESULT 779
ID ADP65315 standard; protein; 688 AA.
DE Human complement C1s component precursor (C1 esterase).
PN W02003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match
Best Local Similarity 8.5%; Score 334; DB 7; Length 688;
PRED. NO. 5.9e-10;
RESULT 780
ID ADU75392 standard; protein; 688 AA.
DE Marker gene related amino acid sequence SEQ ID NO:644.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match
Best Local Similarity 8.5%; Score 334; DB 8; Length 688;
PRED. NO. 5.9e-10;
RESULT 781
ID ADJ91020 standard; protein; 688 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:6.
PN W02004024925-A2.
PD 25-MAR-2004.
PA (NART-) NATIMUNE AS.
Query Match
Best Local Similarity 8.5%; Score 334; DB 8; Length 688;
PRED. NO. 5.9e-10;
RESULT 782

ID AEM81337 standard; protein: 688 AA.
DE Tumor-associated antigenic target (TAT) polypeptide PRO2660, SEQ:3453.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 334; DB 8; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.9e-10;
RESULT 783
ID ADU06459 standard; protein: 688 AA.
DE Human bronchial cancer-associated human protein SeqID683.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 8.5%; Score 334; DB 8; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.9e-10;
RESULT 784
ID ADX26285 standard; protein: 688 AA.
DE Novel cell pain response detection method-related human protein SeqID631.
PN WO2005014845-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match 8.5%; Score 334; DB 9; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.9e-10;
RESULT 785
ID AD280432 standard; protein: 688 AA.
DE Mature complement C1s (C1 esterase) SEQ ID NO 45.
PN WO2005040422-A2.
PD 06-MAY-2005.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match 8.5%; Score 334; DB 9; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.9e-10;
RESULT 786
ID AEB74705 standard; protein: 688 AA.
DE Human placental protein SEQ ID NO:1533.
PN US200555114-A1.
PD 17-NOV-2005.
PA (NOVE-) NUVELO INC.
Query Match 8.5%; Score 334; DB 9; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.9e-10;
RESULT 787
ID AEX17066 standard; protein: 688 AA.
DE Human C1s fragment SEQ ID NO 821.
PN WO2005072340-A2.
PD 11-AUG-2005.
PA (COMP-) COMPUGEN LTD.
PA (COMP-) COMPUGEN INC.
Query Match 8.5%; Score 334; DB 10; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.9e-10;
RESULT 788
ID AD116884 standard; protein: 855 AA.
DE Human NOVX protein homologue SeqID 420.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.4%; Score 332; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 9.3e-10;
RESULT 789
ID AD116818 standard; protein: 855 AA.
DE Human NOVX protein homologue SeqID 354.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.4%; Score 332; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 9.3e-10;
RESULT 790
ID AEF27702 standard; protein: 855 AA.
DE Human prostamlin, SEQ:132.
PN US2006009634-A1.
PD 12-JAN-2006.
PA (KEKU/) KEKUDA R.

PA (ALSO/) ALSOBROOK J.
PA (TCH/) TCHERNY V.
PA (LITX/) LIT X.
PA (SPYT/) SPYTEK K.
PA (PATT/) PATTURAJAN M.
PA (GROS/) GROSSE W.
PA (LEPL/) LEPELEY D.
PA (BURG/) BURGESS C.
PA (VERN/) VERNET C.
PA (LITL/) LI L.
PA (GORM/) GORMAN L.
PA (EDIN/) EDINGER S.
PA (SCIO/) SCIORE P.
PA (ELER/) EILERMAN K.
PA (MALY/) MALYANKAR U.
PA (ROTH/) ROTHENBERG M.
PA (STON/) STONE D.
PA (BOLD/) BOLDOG F.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S.
PA (ANDE/) ANDERSON D.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R.
PA (MILL/) MILLER C.
PA (EISE/) EISEN A.
Query Match 8.4%; Score 332; DB 10; Length 855;
Best Local Similarity 21.6%; Pred. No. 9.3e-10;
RESULT 791
ID AAE06940 standard; protein: 1019 AA.
DE Human enterokinase protein.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match 8.4%; Score 331.5; DB 4; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.2e-09;
RESULT 792
ID ADA83985 standard; protein: 1019 AA.
DE Human PRSS7 protein.
PN WO2002103028-A2.
PD 27-DEC-2002.
PA (BIOM-) BIOMEDICAL CENT.
Query Match 8.4%; Score 331.5; DB 6; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.2e-09;
RESULT 793
ID AD110400 standard; protein: 1019 AA.
DE Human cell surface protease #16.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.4%; Score 331.5; DB 7; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.2e-09;
RESULT 794
ID ADJ46924 standard; protein: 1019 AA.
DE Human transmembrane serine protease (MTSP)-related polypeptide #6.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 8.4%; Score 331.5; DB 8; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.2e-09;
RESULT 795
ID AAE25673 standard; protein: 1019 AA.
DE Human serine protease PRSS7 SEQ ID NO 18.
PN WO2005110338-A2.
PD 24-NOV-2005.
PA (GANY-) GANYMED PHARM AG.
Query Match 8.4%; Score 331.5; DB 10; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.2e-09;
RESULT 796
ID AAE83015 standard; protein: 1019 AA.
DE Human enteropeptidase.
PN WO2006050999-A2.
PD 18-MAY-2006.
PA (OBER-) OBE THERAPY BIOTECHNOLOGY SAS.

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Query Match      8.4%; Score 331.5; DB 10; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.2e-09;
RESULT 797
ID ADU70437 standard; protein, 1019 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID2243.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match      8.4%; Score 330.5; DB 7; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.3e-09;
RESULT 798
ID ADU70480 standard; protein, 3389 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID2286.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match      8.4%; Score 329.5; DB 7; Length 3389;
Best Local Similarity 20.8%; Pred. No. 4.6e-09;
RESULT 799
ID ABE02790 standard; protein, 3566 AA.
DE Human S-100 beta binding protein, SEQ ID NO:33.
PN WO2005106473-A1.
PD 10-NOV-2005.
PA (ONOX) ONO PHARM CO LTD.
Query Match      8.4%; Score 329.5; DB 9; Length 3566;
Best Local Similarity 20.8%; Pred. No. 4.8e-09;
RESULT 800
ID ADH72216 standard; protein, 3567 AA.
DE Human protein of the invention NOV54b SEQ ID NO:1112.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match      8.4%; Score 329.5; DB 8; Length 3567;
Best Local Similarity 20.8%; Pred. No. 4.8e-09;
RESULT 801
ID AAR13623 standard; protein, 460 AA.
DE Human Protein C zymogen SC.
PN EP43875-A.
PD 28-AUG-1991.
PA (LILLY) LILLY & CO ELI.
Query Match      8.3%; Score 329; DB 2; Length 460;
Best Local Similarity 25.5%; Pred. No. 7.6e-10;
RESULT 802
ID ABG76507 standard; protein, 1274 AA.
DE DNA encoding protein modification and maintenance molecule #11.
PN WO200260942-A2.
PD 08-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match      8.3%; Score 328.5; DB 5; Length 1274;
Best Local Similarity 20.8%; Pred. No. 2.1e-09;
RESULT 803
ID AAU11815 standard; protein, 1783 AA.
DE Cancer and neurogenesis associated gene, variant 5G-3V3.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match      8.3%; Score 328.5; DB 5; Length 1783;
Best Local Similarity 20.8%; Pred. No. 2.9e-09;
RESULT 804
ID AAU11813 standard; protein, 1800 AA.
DE Cancer and neurogenesis associated gene, variant 5G-3V1.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match      8.3%; Score 328.5; DB 5; Length 1800;
Best Local Similarity 20.8%; Pred. No. 2.9e-09;
RESULT 805
ID AAU11812 standard; protein, 1826 AA.
DE Cancer and neurogenesis associated gene.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match      8.3%; Score 328.5; DB 5; Length 1826;
Best Local Similarity 20.8%; Pred. No. 2.9e-09;
RESULT 806
ID AAU11814 standard; protein, 2008 AA.
DE Cancer and neurogenesis associated gene, variant 5G-3V2.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match      8.3%; Score 328.5; DB 5; Length 2008;
Best Local Similarity 20.8%; Pred. No. 3.2e-09;
RESULT 807
ID AAU11817 standard; protein, 2306 AA.
DE Cancer and neurogenesis associated gene, variant 5R23V2.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match      8.3%; Score 328.5; DB 5; Length 2306;
Best Local Similarity 20.8%; Pred. No. 3.6e-09;
RESULT 808
ID AAU11816 standard; protein, 2352 AA.
DE Cancer and neurogenesis associated gene, variant 5R-3V2.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEEDS.
Query Match      8.3%; Score 328.5; DB 5; Length 2352;
Best Local Similarity 20.8%; Pred. No. 3.7e-09;
RESULT 809
ID AAB19551 standard; protein, 683 AA.
DE Human matrilipase (truncated form).
PN WO20005332-A1.
PD 14-SEP-2000.
PA (GEOU) UNIV GEORGETOWN.
Query Match      8.3%; Score 328; DB 3; Length 683;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 810
ID AAY90284 standard; protein, 762 AA.
DE Human peptidase, HEP-1 protein sequence.
PN WO200042301-A2.
PD 20-JUL-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match      8.3%; Score 328; DB 3; Length 762;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 811
ID AAM25628 standard; protein, 851 AA.
DE Human protein sequence SEQ ID NO:1143.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match      8.3%; Score 328; DB 4; Length 851;
Best Local Similarity 21.6%; Pred. No. 1.5e-09;
RESULT 812
ID ABB1428 standard; peptide, 851 AA.
DE Human membrane-type Ser kinase homologue, SEQ ID NO:1798.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match      8.3%; Score 328; DB 4; Length 851;
Best Local Similarity 21.6%; Pred. No. 1.5e-09;
RESULT 813
ID ADO55145 standard; protein, 853 AA.
DE Protein #47 with increased gene expression in renal cell carcinoma.
PN WO2000603842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match      8.3%; Score 328; DB 8; Length 853;
Best Local Similarity 21.4%; Pred. No. 1.5e-09;
RESULT 814
ID AAB19552 standard; protein, 855 AA.
DE Human matrilipase.
PN WO20005332-A1.
PD 14-SEP-2000.
PA (GEOU) UNIV GEORGETOWN.
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Query Match 8.3%; Score 328; DB 3; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.5e-09;
RESULT 815
ID AAB35465 standard; protein; 855 AA.
DE Human membrane-type serine protease MT-Sp1.
PN WO200123524-A2.
PD 05-APR-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 8.3%; Score 328; DB 4; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.5e-09;
RESULT 816
ID AD116817 standard; protein; 855 AA.
DE Human NOVX protein homologue SegID 353.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 328; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.5e-09;
RESULT 817
ID AD116883 standard; protein; 855 AA.
DE Human NOVX protein homologue SegID 419.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 328; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.5e-09;
RESULT 818
ID AD116876 standard; protein; 855 AA.
DE Human NOVX protein homologue SegID 412.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 328; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.5e-09;
RESULT 819
ID ADN39867 standard; protein; 855 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SRQ ID NO:C237.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.3%; Score 328; DB 7; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.5e-09;
RESULT 820
ID ADN04754 standard; protein; 855 AA.
DE Antisporiatic protein sequence #558.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 8.3%; Score 328; DB 8; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.5e-09;
RESULT 821
ID ADP23334 standard; protein; 855 AA.
DE PRO polypeptide SEQ ID NO:428.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 8.3%; Score 328; DB 8; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.5e-09;
RESULT 822
ID AE146688 standard; protein; 855 AA.
DE Human cancer-associated protease Matrilptase.
PN WO2006068975-A2.
PD 29-JUN-2006.
PA (ABGE-) ABGENIX INC.
Query Match 8.3%; Score 328; DB 10; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.5e-09;
RESULT 823
ID ABR66721 standard; protein; 863 AA.
DE Human prostatic carcinoma derived protein SEQ ID 233 #3.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.

PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 8.3%; Score 328; DB 8; Length 863;
Best Local Similarity 21.4%; Pred. No. 1.5e-09;
RESULT 824
ID ADR66379 standard; protein; 863 AA.
DE Human prostatic carcinoma derived protein SEQ ID 233 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 8.3%; Score 328; DB 8; Length 863;
Best Local Similarity 21.4%; Pred. No. 1.5e-09;
RESULT 825
ID AAB58274 standard; protein; 449 AA.
DE Lung cancer associated polypeptide sequence SEQ ID 612.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 8.3%; Score 327.5; DB 3; Length 449;
Best Local Similarity 23.3%; Pred. No. 8.9e-10;
RESULT 826
ID ADL64961 standard; protein; 688 AA.
DE Human complement component 1 protein, CIS.
PN US2004033582-A1.
PD 19-FEB-2004.
PA (EDMO/) EDMONDS M.
PA (HUI/) HUI L.
PA (PERR/) PERRONE M.
PA (POWE/) POWELL J R.
PA (RAMA/) RAMANATHAN C S.
PA (SWAN/) SWANSON B.
PA (TSUC/) TSUCHIHASHI Z.
PA (ZERR/) ZERRBA K.
Query Match 8.3%; Score 327; DB 8; Length 688;
Best Local Similarity 21.7%; Pred. No. 1.4e-09;
RESULT 827
ID AD116508 standard; protein; 757 AA.
DE Human NOVX protein to treat human pathological conditions SegID44.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 327; DB 5; Length 757;
Best Local Similarity 21.6%; Pred. No. 1.5e-09;
RESULT 828
ID AAY06671 standard; protein; 855 AA.
DE Tumour antigen derived gene-15 (TADG-15) protein.
PN WO9942120-A1.
PD 26-AUG-1999.
PA (UYAR-) UNIV ARKANSAS.
Query Match 8.3%; Score 327; DB 2; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 829
ID AAB98500 standard; protein; 855 AA.
DE Human TADG-15.
PN WO200129056-A1.
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Query Match 8.3%; Score 327; DB 4; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 830
ID AAE06930 standard; protein; 855 AA.
DE Human membrane-type serine protease (MTSP) 1.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 4; Length 855;

Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 831
ID AAO22929 standard; protein; 855 AA.
DE Type II transmembrane serine protease 1 protein SEQ ID NO 2.
PN WO200272786-A2.
PD 19-SEP-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 832
ID ADI16816 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 352.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 833
ID ADI16882 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 418.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 834
ID ADI16875 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 411.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 835
ID ABB5619 standard; protein; 855 AA.
DE Human membrane-type serine protease MTSP1 protein SEQ ID NO:2.
PN WO200292841-A2.
PD 21-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 836
ID AAO30146 standard; protein; 855 AA.
DE Human membrane-type serine protease MTSP1 protein.
PN WO2003044179-A2.
PD 30-MAY-2003.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 837
ID AAE29820 standard; protein; 855 AA.
DE Human membrane-type serine protease 1 (MTSP1).
PN WO20027287-A2.
PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 838
ID AAE29791 standard; protein; 855 AA.
DE Human membrane-type serine protease, MTSP1.
PN WO20027287-A2.
PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 839
ID ABB72376 standard; protein; 855 AA.
DE Transmembrane serine protease 1 (MTSP1).
PN WO2003004681-A2.
PD 16-JAN-2003.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 6; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;

RESULT 840
ID ADB97551 standard; protein; 855 AA.
DE Human MTSP1, SEQ ID NO:2.
PN WO2003031585-A2.
PD 17-APR-2003.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 7; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 841
ID ADI10371 standard; protein; 855 AA.
DE Human cell surface protease #1.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 7; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 842
ID ADG65326 standard; protein; 855 AA.
DE Human MTSP1.
PN WO2003104394-A2.
PD 18-DEC-2003.
PA (DENB-) DENBREON SAN DIEGO LLC.
Query Match 8.3%; Score 327; DB 8; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 843
ID ADI28861 standard; protein; 855 AA.
DE Human matrixase (MTSP1) serine protease.
PN WO2004005471-A2.
PD 15-JAN-2004.
PA (DENB-) DENBREON SAN DIEGO LLC.
Query Match 8.3%; Score 327; DB 8; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 844
ID ADJ46895 standard; protein; 855 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #1.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 8; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 845
ID AEB61724 standard; protein; 855 AA.
DE Human membrane-type serine protease 1.
PN WO2005100556-A2.
PD 27-OCT-2005.
PA (CATALY-) CATALYST BIOSCIENCES.
Query Match 8.3%; Score 327; DB 9; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 846
ID AEE05739 standard; protein; 855 AA.
DE Wild type human membrane-type serine protease 1 (MT-Sp1).
PN WO2005110453-A2.
PD 24-NOV-2005.
PA (CATALY-) CATALYST BIOSCIENCES.
Query Match 8.3%; Score 327; DB 9; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.7e-09;
RESULT 847
ID AAE20788 standard; protein; 3095 AA.
DE Rat C3b/C4b complement receptor like protein.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.2%; Score 324; DB 5; Length 3095;
Best Local Similarity 20.1%; Pred. No. 8.3e-09;
RESULT 848
ID ADN42162 standard; protein; 757 AA.
DE Human novel protein NOV 8.
PN US2004033493-A1.
PD 19-FEB-2004.
PA (TCHE-) TCHEKNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATV/) PATURAJAN M.

PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (GANG/) GANCOLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENNA C E A.
PA (FURT/) FURTA K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
Query Match
Best Local Similarity 8.1%; Score 323; DB 8; Length 757;
Pred. No. 2.5e-09;
RESULT 849
ID ADH71146 standard; protein; 3130 AA.
DE Human protein of the invention NOV4f SEQ ID NO:42.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 321; DB 8; Length 3130;
Pred. No. 1.2e-08;
RESULT 850
ID ADH71144 standard; protein; 3483 AA.
DE Human protein of the invention NOV4e SEQ ID NO:40.
PN WO2003102155-A2..
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 321; DB 8; Length 3483;
Pred. No. 1.4e-08;
RESULT 851
ID ADH71136 standard; protein; 3546 AA.
DE Human protein of the invention NOV4a SEQ ID NO:32.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 321; DB 8; Length 3546;
Pred. No. 1.4e-08;
RESULT 852
ID AAE20787 standard; protein; 3069 AA.
DE Human C3b/C4b complement receptor like protein #1.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 8.1%; Score 320.5; DB 5; Length 3069;
Pred. No. 1.3e-08;
RESULT 853
ID AAE20789 standard; protein; 3100 AA.
DE Human C3b/C4b complement receptor like protein #2.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 8.1%; Score 320.5; DB 5; Length 3100;
Pred. No. 1.3e-08;
RESULT 854
ID AAU99088 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant G383N/G385T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 8.1%; Score 319.5; DB 5; Length 419;
Pred. No. 2.3e-09;
RESULT 855
ID AAU99080 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L349N/D351T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 8.1%; Score 318; DB 8; Length 2669;
Pred. No. 1.5e-08;
RESULT 860
ID ADH71140 standard; protein; 2669 AA.
DE Human protein of the invention NOV4c SEQ ID NO:36.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 318; DB 8; Length 2669;
Pred. No. 1.5e-08;
RESULT 861
ID AEG79168 standard; protein; 3104 AA.
DE Human cub and sushi domain containing protein #1.
PN WO200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 318; DB 5; Length 3104;
Pred. No. 1.8e-08;
RESULT 862
ID ADH71168 standard; protein; 3104 AA.
DE Human protein of the invention NOV4q SEQ ID NO:64.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 318; DB 8; Length 3104;
Pred. No. 1.8e-08;
RESULT 863
ID ADH71166 standard; protein; 3104 AA.
DE Human protein of the invention NOV4p SEQ ID NO:62.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.1%; Score 318; DB 8; Length 3104;
Pred. No. 1.8e-08;
RESULT 864
ID ADH71138 standard; protein; 3104 AA.

DE Human protein of the invention NOV4b SEQ ID NO:34.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.8e-08;
RESULT 865
ID AAU99006 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D189N/K191T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 317.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 2.9e-09;
RESULT 866
ID AAU99066 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T315N/V317T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 317.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.9e-09;
RESULT 867
ID ADM28524 standard; protein; 421 AA.
DE Human Protein C variant #2.
PN W02004113385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 317.5; DB 9; Length 421;
Best Local Similarity 24.7%; Pred. No. 2.9e-09;
RESULT 868
ID AAR20987 standard; protein; 627 AA.
DE Novel human polypeptide SEQ ID NO 1681.
PN W02005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 8.0%; Score 317.5; DB 9; Length 627;
Best Local Similarity 21.3%; Pred. No. 4.2e-09;
RESULT 869
ID AAR57283 standard; protein; 798 AA.
DE Bovine enterokinase.
PN W09416083-A1.
PD 21-JUL-1994.
PA (GENY-) GENETICS INST INC.
Query Match 8.0%; Score 317.5; DB 2; Length 798;
Best Local Similarity 24.6%; Pred. No. 5.3e-09;
RESULT 870
ID AAE20900 standard; protein; 3069 AA.
DE Human C3b/C4b complement receptor like protein #1, alternative version.
PN W0200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.0%; Score 317.5; DB 5; Length 3069;
Best Local Similarity 20.7%; Pred. No. 1.9e-08;
RESULT 871
ID AAE20901 standard; protein; 3100 AA.
DE Human C3b/C4b complement receptor like protein #2, alternative version.
PN W0200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.0%; Score 317.5; DB 5; Length 3100;
Best Local Similarity 20.7%; Pred. No. 1.9e-08;
RESULT 872
ID AAU99076 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant M38N/S340T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 316.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 873
ID AAU99071 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S336N/M338S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 3.7e-09;
RESULT 874
ID AAU99026 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L220N/R222T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 875
ID AAU99081 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D351N/Q353S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 876
ID AAU99071 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S336N/M338S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 3.7e-09;
RESULT 877
ID AAU99087 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant G383N/G385S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 878
ID AAU99079 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L349N/D351S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 2; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 879
ID AAR62653 standard; protein; 461 AA.
DE Human Protein C.
PN US358932-A.
PD 25-OCT-1994.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 880
ID AAR35760 standard; protein; 419 AA.
DE Protein C (PC).
PN W09309804-A1.
PD 27-MAY-1993.
PA (SCRI-) SCRIPPS RES INST.
Query Match 8.0%; Score 314.5; DB 2; Length 419;
Best Local Similarity 23.3%; Pred. No. 4.2e-09;
RESULT 881
ID AAU99053 standard; protein; 419 AA.

Best Local Similarity 24.7%; Pred. No. 3.3e-09;
RESULT 873
ID AAU99022 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K217N/L219T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 316.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.3e-09;
RESULT 874
ID AAU99026 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L220N/R222T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 875
ID AAU99081 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D351N/Q353S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 876
ID AAU99071 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S336N/M338S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 3.7e-09;
RESULT 877
ID AAU99087 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant G383N/G385S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 878
ID AAU99079 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L349N/D351S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 2; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 879
ID AAR62653 standard; protein; 461 AA.
DE Human Protein C.
PN US358932-A.
PD 25-OCT-1994.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match 8.0%; Score 315.5; DB 5; Length 461;
Best Local Similarity 24.5%; Pred. No. 4e-09;
RESULT 880
ID AAR35760 standard; protein; 419 AA.
DE Protein C (PC).
PN W09309804-A1.
PD 27-MAY-1993.
PA (SCRI-) SCRIPPS RES INST.
Query Match 8.0%; Score 314.5; DB 2; Length 419;
Best Local Similarity 23.3%; Pred. No. 4.2e-09;
RESULT 881
ID AAU99053 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant R306N/K308S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 4.2e-09;
RESULT 892
ID AAU99007 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S190N/K192S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 4.2e-09;
RESULT 893
ID AAU99077 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant I348N/G350S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.2e-09;
RESULT 894
ID AAU99043 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L296N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.2e-09;
RESULT 895
ID ADG83832 standard; protein; 454 AA.
DE Red belly black snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match 8.0%; Score 314.5; DB 8; Length 454;
Best Local Similarity 23.0%; Pred. No. 4.5e-09;
RESULT 896
ID ADM77504 standard; protein; 461 AA.
DE Human protein C variant #2 amino acid sequence.
PN WO200310666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 314.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 4.6e-09;
RESULT 897
ID ADM28523 standard; protein; 420 AA.
DE Human protein C variant #1.
PN WO2004113385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 314; DB 9; Length 420;
Best Local Similarity 24.5%; Pred. No. 4.5e-09;
RESULT 898
ID AAE23083 standard; protein; 855 AA.
DE Epitich protein.
PN WO200203787-A2.
PD 17-JAN-2002.
PA (DELT-) DELTAGEN INC.
Query Match 8.0%; Score 314; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 8.7e-09;
RESULT 899
ID ADL16819 standard; protein; 855 AA.
DE Murine NOVX protein homologue Segid 355.
PN WO200268649-A2.
PD 06-SEP-2002.

PA (CURA-) CURAGEN CORP.
Query Match 8.0%; Score 314; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 8.7e-09;
RESULT 890
ID ADL16877 standard; protein; 855 AA.
DE Murine NOVX protein homologue Segid 413.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.0%; Score 314; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 8.7e-09;
RESULT 891
ID AAW72753 standard; protein; 419 AA.
DE Primary structure of activated human protein C.
PN EP875563-A2.
PD 04-NOV-1998.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 313.5; DB 2; Length 419;
Best Local Similarity 23.3%; Pred. No. 4.7e-09;
RESULT 892
ID AAU99005 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D189N/K191S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 893
ID AAU99025 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L220N/R222S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 894
ID AAU99065 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T315N/V317S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.3%; Pred. No. 4.7e-09;
RESULT 895
ID AAU99016 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D214N/S216T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 4.7e-09;
RESULT 896
ID AAU99023 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K218N/L220S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 897
ID AEA44151 standard; protein; 419 AA.
DE Human protein C analog with A264I substitution.
PN WO2006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 313.5; DB 10; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 898

ID AAR1083 standard; protein; 509 AA.
DE PAP-I-protein C fusion construct.
PN MO9109953-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 313; DB 2; Length 509;
Best Local Similarity 23.5%; Pred. No. 6e-09;
RESULT 899
ID AD116820 standard; protein; 855 AA.
DE Rat NOVX protein homologue SeqID 356.
PN MO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 9.8e-09;
RESULT 900
ID AD116881 standard; protein; 855 AA.
DE Rat NOVX protein homologue SeqID 417.
PN MO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 9.8e-09;
RESULT 901
ID AD116878 standard; protein; 855 AA.
DE Rat NOVX protein homologue SeqID 414.
PN MO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 9.8e-09;
RESULT 902
ID AAU99072 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S336N/M338T.
PN MO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 903
ID AAU99097 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D189N/K191N.
PN MO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 904
ID AAU99009 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K191N/K193S.
PN MO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 5.4e-09;
RESULT 905
ID AAU99064 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R312N/R314T.
PN MO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.9%; Pred. No. 5.4e-09;
RESULT 906
ID AAU99069 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V334N.
PN MO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 907
ID AAU99082 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D351N/Q353T.
PN MO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 908
ID AAU99096 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant M338A.
PN MO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 909
ID AAU99091 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L387N/N389S.
PN MO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 910
ID AAU99024 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K218N/L220T.
PN MO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 911
ID AAU99048 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H303N/S305T.
PN MO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 912
ID AAU99067 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant F316N/L318S.
PN MO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.3%; Pred. No. 5.4e-09;
RESULT 913
ID AAU99075 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant M338N.
PN MO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 914
ID AAU99092 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L387N/N389T.
PN MO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.4e-09;
RESULT 915
ID AAU99092 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L387N/N389T.
PN MO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.

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Query Match
Best Local Similarity 7.9%; Score 312.5; DB 5; Length 419;
RESULT 915
ID AAU99011 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K192N/L194S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 312.5; DB 5; Length 419;
RESULT 916
ID AAU99032 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S250N/S252T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 312.5; DB 5; Length 419;
RESULT 917
ID ADM77507 standard; protein; 461 AA.
DE Human protein C variant #5 amino acid sequence.
PN WO200310666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 312.5; DB 8; Length 461;
RESULT 918
ID ADM77505 standard; protein; 461 AA.
DE Human protein C variant #3 amino acid sequence.
PN WO200310666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 312.5; DB 8; Length 461;
RESULT 919
ID AEK16852 standard; protein; 622 AA.
DE Human HUMCIRS P6 protein SEQ ID NO 95.
PN WO2005072340-A2.
PD 11-AUG-2005.
PA (COMP-) COMPUGEN LTD.
PA (COMP-) COMPUGEN INC.
Query Match
Best Local Similarity 7.9%; Score 312.5; DB 10; Length 622;
RESULT 920
ID AEK17063 standard; protein; 622 AA.
DE Human HUMCIRS_PEA_1_P22 protein fragment SEQ ID NO 818.
PN WO2005072340-A2.
PD 11-AUG-2005.
PA (COMP-) COMPUGEN LTD.
PA (COMP-) COMPUGEN INC.
Query Match
Best Local Similarity 7.9%; Score 312.5; DB 10; Length 622;
RESULT 921
ID AAB82677 standard; protein; 419 AA.
DE Human protein C derivative (H100/S11G/Q32E/N33D/L194S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 312; DB 4; Length 419;
RESULT 922
ID AAR13537 standard; protein; 460 AA.
DE Human Protein C zymogen N.
PN EP43875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 312; DB 2; Length 460;
RESULT 923
ID AAB82677 standard; protein; 419 AA.
DE Coeatal taiipan venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match
Best Local Similarity 7.9%; Score 312; DB 8; Length 467;
RESULT 924
ID ABP60993 standard; protein; 1031 AA.
DE Novel human protein. SEQ ID 80.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAXO) GLAXO GROUP LTD.
Query Match
Best Local Similarity 7.9%; Score 312; DB 5; Length 1031;
RESULT 925
ID AAU99008 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S190N/K192T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 311.5; DB 5; Length 419;
RESULT 926
ID AAU99039 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T254N/N256S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 311.5; DB 5; Length 419;
RESULT 927
ID AAU99047 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H303N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 311.5; DB 5; Length 419;
RESULT 928
ID AAU99070 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V334N/S336T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 311.5; DB 5; Length 419;
RESULT 929
ID AAU99017 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E215N/K217S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 311.5; DB 5; Length 419;
RESULT 930
ID AAU99044 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L296N/T298S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 311.5; DB 5; Length 419;
RESULT 931
ID AAU99014 standard; protein; 419 AA.
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DE Human Protein C zymogen protein mutant K193N/A195T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.1e-09;
RESULT 932
ID AAU99031 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant S250N.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.1e-09;
RESULT 933
ID AAU99057 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant K306N/A310S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.1e-09;
RESULT 934
ID AAU99054 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant R306N/K308T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.1e-09;
RESULT 935
ID AAU99095 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant D214A.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.1e-09;
RESULT 936
ID AAU99015 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant D214N.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.1e-09;
RESULT 937
ID AAP81205 standard; protein: 461 AA.
DE Human protein C.
PN EP266190-A.
PD 04-MAY-1988.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 311.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.6e-09;
RESULT 938
ID AAR13539 standard; protein: 461 AA.
DE Human Protein C zymogen LIN.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.6e-09;
RESULT 939
ID AAR13997 standard; protein: 461 AA.
DE Human protein C zymogen Q329.
PN EP443874-A.
PD 28-AUG-1991.

PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.6e-09;
RESULT 940
ID ADM77503 standard; protein: 461 AA.
DE Human protein C variant #1 amino acid sequence.
PN W0200310666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.6e-09;
RESULT 941
ID AAB82678 standard; protein: 419 AA.
DE Human protein C derivative (H100/S11G/Q32E/N33D/L194S/T254S).
PN W0200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.5e-09;
RESULT 942
ID AAB82675 standard; protein: 419 AA.
DE Human protein C derivative (S11G/Q32E/N33D/L194S).
PN W0200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.5e-09;
RESULT 943
ID ADX39090 standard; protein: 446 AA.
DE Rat factor VII.
PN W02005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.9%; Score 311; DB 9; Length 446;
Best Local Similarity 23.3%; Pred. No. 6.8e-09;
RESULT 944
ID ADC40013 standard; protein: 409 AA.
DE Human activated protein C-related protein #2.
PN W02003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 409;
Best Local Similarity 24.5%; Pred. No. 6.7e-09;
RESULT 945
ID ADC40012 standard; protein: 410 AA.
DE Human activated protein C-related protein #1.
PN W02003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 410;
Best Local Similarity 24.5%; Pred. No. 6.7e-09;
RESULT 946
ID AA156803 standard; protein: 415 AA.
DE Truncated human protein C polypeptide.
PN W09963070-A1.
PD 09-DEC-1999.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 3; Length 415;
Best Local Similarity 24.5%; Pred. No. 6.8e-09;
RESULT 947
ID AAB82673 standard; protein: 419 AA.
DE Wild-type human protein C.
PN W0200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 948
ID AAB36896 standard; protein: 419 AA.
DE Human protein C derivative 3.
PN W0200066754-A1.
PD 09-NOV-2000.

PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 949
ID AAB36894 standard; protein; 419 AA.
DE Human protein C derivative 1.
PN W020006754-A1.
PD 09-NOV-2000.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 950
ID AAE08625 standard; protein; 419 AA.
DE Human mature wild type protein C.
PN W0200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 951
ID AAU99063 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R312N/R314S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 952
ID AAU99012 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K192N/L194T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 953
ID AAU99050 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S304N/R306T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 954
ID AAU99010 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K191N/K193T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 6.9e-09;
RESULT 955
ID AAU99040 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T254N/N256T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 956
ID AAU99060 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E309N/K311T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;

RESULT 957
ID AAU99055 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E307N/E309S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 958
ID AAU99056 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E307N/E309T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 959
ID AAU99059 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E309N/K311S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 960
ID AAU99002 standard; protein; 419 AA.
DE Human Protein C zymogen protein.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 961
ID AAU99051 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 962
ID AAU99052 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 963
ID ABR55547 standard; protein; 419 AA.
DE Amino acid sequence of mature human protein C (PC).
PN FR2831170-A1.
PD 25-APR-2003.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 7.9%; Score 310.5; DB 6; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 964
ID ADC40014 standard; protein; 419 AA.
DE Human activated protein C-related protein #3.
PN W02003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
RESULT 965
ID ADO16786 standard; protein; 419 AA.
DE Mature human zymogen-like protein C.

PN WO200404190-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 8; Length 419;
Pred. No. 6.9e-09;
RESULT 966
ID ADM28521 standard; protein; 419 AA.
DE Human protein C.
PN WO2004113385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 9; Length 419;
Pred. No. 6.9e-09;
RESULT 967
ID ADY52283 standard; protein; 419 AA.
DE Human activated protein C (APC).
PN WO2005023308-A1.
PD 17-MAR-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 9; Length 419;
Pred. No. 6.9e-09;
RESULT 968
ID AEH44147 standard; protein; 419 AA.
DE Human protein C analog with S3Y substitution.
PN WO2006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 10; Length 419;
Pred. No. 6.9e-09;
RESULT 969
ID AEH44149 standard; protein; 419 AA.
DE Human protein C analog with L8M substitution.
PN WO2006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 10; Length 419;
Pred. No. 6.9e-09;
RESULT 970
ID AEH44146 standard; protein; 419 AA.
DE Wild-type human protein C zymogen.
PN WO2006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 10; Length 419;
Pred. No. 6.9e-09;
RESULT 971
ID AEH44148 standard; protein; 419 AA.
DE Human protein C analog with S3F substitution.
PN WO2006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 10; Length 419;
Pred. No. 6.9e-09;
RESULT 972
ID AEA44154 standard; protein; 419 AA.
DE Human protein C analog with V375I substitution.
PN WO2006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 10; Length 419;
Pred. No. 6.9e-09;
RESULT 973
ID ADG83834 standard; protein; 453 AA.
DE Mainland tiger snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 8; Length 453;
Pred. No. 7.4e-09;
RESULT 974

ID AAP81104 standard; protein; 460 AA.
DE Sequence of human protein C.
PN JP63263083-A.
PD 31-OCT-1988.
PA (FAKH) HOECHST JAPAN LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 1; Length 460;
Pred. No. 7.5e-09;
RESULT 975
ID AAW25086 standard; protein; 460 AA.
DE Human protein C.
PN WO9720043-A1.
PD 05-JUN-1997.
PA (ZYMO) ZYMOGENETICS INC.
PA (PPLT-) PPL THERAPEUTICS.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 2; Length 460;
Pred. No. 7.5e-09;
RESULT 976
ID AAP60001 standard; protein; 461 AA.
DE Sequence of polypeptide with human protein C activity.
PN EP191606-A.
PD 20-AUG-1986.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 1; Length 461;
Pred. No. 7.5e-09;
RESULT 977
ID AAP70855 standard; protein; 461 AA.
DE Human protein C.
PN EP215548-A.
PD 25-MAR-1987.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 1; Length 461;
Pred. No. 7.5e-09;
RESULT 978
ID AAP90401 standard; protein; 461 AA.
DE Zymogen form of human protein C.
PN EP323149-A.
PD 05-JUL-1989.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 1; Length 461;
Pred. No. 7.5e-09;
RESULT 979
ID AAR13622 standard; protein; 461 AA.
DE Human protein C.
PN WO9112320-A.
PD 22-AUG-1991.
PA (ZYMO) ZYMOGENETICS INC.
PA (TEIJ) TEIJIN LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 2; Length 461;
Pred. No. 7.5e-09;
RESULT 980
ID AAR13081 standard; protein; 461 AA.
DE Human protein C.
PN WO9109953-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 2; Length 461;
Pred. No. 7.5e-09;
RESULT 981
ID AAR13074 standard; protein; 461 AA.
DE Protein C precursor.
PN WO9109951-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
PA (TEIJ) TEIJIN LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 2; Length 461;
Pred. No. 7.5e-09;
RESULT 982
ID AAR34295 standard; protein; 461 AA.
DE Protein C.
PN JP05064588-A.
PD 19-MAR-1993.
PA (TEIJ) TEIJIN LTD.

Query Match	7.9%	Score 310.5;	DB 2;	Length 461;
Best Local Similarity	24.5%	Pred. No. 7.5e-09;		
RESULT 983				
ID AAW02600 standard; protein; 461 AA.				
DE Human protein C.				
PN US5516650-A.				
PD 14-MAY-1996.				
PA (Zymo) ZymoGenetics Inc.				
Query Match	7.9%	Score 310.5;	DB 2;	Length 461;
Best Local Similarity	24.5%	Pred. No. 7.5e-09;		
RESULT 984				
ID AAY49561 standard; protein; 461 AA.				
DE Human lecithin cholesterol acyltransferase protein sequence.				
PN WO9505454-A2.				
PD 07-OCT-1999.				
PA (WHEB) WHITEHEAD INST. BIOMEDICAL RES.				
Query Match	7.9%	Score 310.5;	DB 2;	Length 461;
Best Local Similarity	24.5%	Pred. No. 7.5e-09;		
RESULT 985				
ID AAB82674 standard; protein; 461 AA.				
DE Wild-type human protein C.				
PN WO200157193-A2.				
PD 09-AUG-2001.				
PA (ELIL) LILLY & CO ELI.				
Query Match	7.9%	Score 310.5;	DB 4;	Length 461;
Best Local Similarity	24.5%	Pred. No. 7.5e-09;		
RESULT 986				
ID AAB36895 standard; protein; 461 AA.				
DE Human protein C derivative 2.				
PN WO20006754-A1.				
PD 09-NOV-2000.				
PA (ELIL) LILLY & CO ELI.				
Query Match	7.9%	Score 310.5;	DB 4;	Length 461;
Best Local Similarity	24.5%	Pred. No. 7.5e-09;		
RESULT 987				
ID AAE08626 standard; protein; 461 AA.				
DE Human wild type protein C.				
PN WO200159084-A1.				
PD 16-AUG-2001.				
PA (ELIL) LILLY & CO ELI.				
Query Match	7.9%	Score 310.5;	DB 4;	Length 461;
Best Local Similarity	24.5%	Pred. No. 7.5e-09;		
RESULT 988				
ID AAU99001 standard; protein; 461 AA.				
DE Human protein C precursor protein.				
PN WO200232461-A2.				
PD 25-APR-2002.				
PA (MAXY-) MAXYGEN APS.				
Query Match	7.9%	Score 310.5;	DB 5;	Length 461;
Best Local Similarity	24.5%	Pred. No. 7.5e-09;		
RESULT 989				
ID ADM77502 standard; protein; 461 AA.				
DE Human protein C wild-type amino acid sequence.				
PN WO200310666-A2.				
PD 24-DEC-2003.				
PA (MAXY-) MAXYGEN APS.				
Query Match	7.9%	Score 310.5;	DB 8;	Length 461;
Best Local Similarity	24.5%	Pred. No. 7.5e-09;		
RESULT 990				
ID ADO18787 standard; protein; 461 AA.				
DE Human zymogen-like protein C.				
PN WO2004044130-A2.				
PD 27-MAY-2004.				
PA (MAXY-) MAXYGEN APS.				
Query Match	7.9%	Score 310.5;	DB 8;	Length 461;
Best Local Similarity	24.5%	Pred. No. 7.5e-09;		
RESULT 991				
ID ADW28520 standard; protein; 461 AA.				
DE Human protein C precursor.				
PN WO2004113385-A1.				
PD 29-DEC-2004.				
PA (MAXY-) MAXYGEN APS.				
Query Match	7.9%	Score 310.5;	DB 9;	Length 461;
Best Local Similarity	24.5%	Pred. No. 7.5e-09;		
RESULT 992				
ID ADM28522 standard; protein; 461 AA.				
DE Human protein C precursor 139R/K mutant.				
PN WO2004113385-A1.				
PD 29-DEC-2004.				
PA (MAXY-) MAXYGEN APS.				
Query Match	7.9%	Score 310.5;	DB 9;	Length 461;
Best Local Similarity	24.5%	Pred. No. 7.5e-09;		
RESULT 993				
ID AEP96684 standard; protein; 461 AA.				
DE Human C-reactive protein (CRP) associated marker SEQ ID NO 866				
PN WO2005107364-A2.				
PD 17-NOV-2005.				
PA (COMP-) COMPUGEN LTD.				
Query Match	7.9%	Score 310.5;	DB 9;	Length 461;
Best Local Similarity	24.5%	Pred. No. 7.5e-09;		
RESULT 994				
ID AEE72258 standard; protein; 461 AA.				
DE Human target protein #99.				
PN WO2005119262-A2.				
PD 15-DEC-2005.				
PA (COHE/) COHEN Y.				
Query Match	7.9%	Score 310.5;	DB 10;	Length 461;
Best Local Similarity	24.5%	Pred. No. 7.5e-09;		
RESULT 995				
ID AEG02811 standard; protein; 461 AA.				

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Best Local Similarity 24.5%; Pred. No. 8.2e-09;
RESULT 1000
ID AEX17219 standard; protein; 557 AA.
DE Human HUMC18s_PEA_1_P22 protein.
PD WO2005072340-A2.
PD 11-AUG-2005.
PA (COMP-) COMPUGEN LTD.
PA (COMP-) COMPUGEN INC.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 10; Length 557;
Pred. No. 9e-09;
RESULT 1001
ID AAB82676 standard; protein; 419 AA.
DE Human protein C derivative (S11G/Q32E/N33D/L194S/7254S).
PD WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310; DB 4; Length 419;
Pred. No. 7.3e-09;
RESULT 1002
ID AAE08630 standard; protein; 419 AA.
DE Human protein C derivative #4.
PD WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310; DB 4; Length 419;
Pred. No. 7.3e-09;
RESULT 1003
ID AAR13538 standard; protein; 460 AA.
DE Human Protein C zymogen FN.
PD EP43875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.9%; Score 310; DB 2; Length 460;
Pred. No. 8e-09;
RESULT 1004
ID AAB36897 standard; protein; 419 AA.
DE Human protein C derivative 4.
PD WO20006754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 4; Length 419;
Pred. No. 7.8e-09;
RESULT 1005
ID AAB36898 standard; protein; 419 AA.
DE Human protein C derivative 5.
PD WO20006754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 4; Length 419;
Pred. No. 7.8e-09;
RESULT 1006
ID AAU99018 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E215N/K217T.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
Pred. No. 7.8e-09;
RESULT 1007
ID AAU99033 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K251N.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
Pred. No. 7.8e-09;
RESULT 1008
ID AAU99013 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K193N/A195S.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
Pred. No. 7.8e-09;
RESULT 1009
ID AAU99068 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant F316N/L318T.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
Pred. No. 7.8e-09;
RESULT 1010
ID AAU99062 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant A310N/R312T.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
Pred. No. 7.8e-09;
RESULT 1011
ID AAU99020 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S216N/K218T.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
Pred. No. 7.8e-09;
RESULT 1012
ID AAU99035 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S252N.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
Pred. No. 7.8e-09;
RESULT 1013
ID AAU99085 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E357N/D359S.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
Pred. No. 7.8e-09;
RESULT 1014
ID AAU99058 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K308N/A310T.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
Pred. No. 7.8e-09;
RESULT 1015
ID AAU99019 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S216N/K218S.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 309.5; DB 5; Length 419;
Pred. No. 7.8e-09;
RESULT 1016
ID AAU99094 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H388N/Y390T.
PD WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
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PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 7.8e-09;
RESULT 1017
ID AAU99089 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L386N/H388S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.8%; Pred. No. 7.8e-09;
RESULT 1018
ID AEH44153 standard; protein; 419 AA.
DE Human protein C analog with Q35R substitution.
PN WO2006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 10; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.8e-09;
RESULT 1019
ID AAP90070 standard; protein; 461 AA.
DE Human protein C.
PN EP319312-A.
PD 07-JUN-1989.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 8.5e-09;
RESULT 1020
ID AAR13540 standard; protein; 461 AA.
DE Human Protein C zymogen FLIN.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 8.5e-09;
RESULT 1021
ID ADI16874 standard; protein; 799 AA.
DE Murine NOVX protein homologue SegID 410.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 309.5; DB 5; Length 799;
Best Local Similarity 21.6%; Pred. No. 1.4e-08;
RESULT 1022
ID ADI16880 standard; protein; 799 AA.
DE Murine NOVX protein homologue SegID 416.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 309.5; DB 5; Length 799;
Best Local Similarity 21.6%; Pred. No. 1.4e-08;
RESULT 1023
ID AAE08627 standard; protein; 419 AA.
DE Human protein C derivative #1.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.3e-09;
RESULT 1024
ID AAE08629 standard; protein; 419 AA.
DE Human protein C derivative #3.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.3e-09;
RESULT 1025
ID AAU99049 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S304N/R306S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (ELIL) LILLY & CO ELI.

PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.8e-09;
RESULT 1026
ID AAU99061 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant A310N/R312S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.1%; Pred. No. 8.8e-09;
RESULT 1027
ID AAU99090 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L386N/H388T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.8e-09;
RESULT 1028
ID AAU99086 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E357N/D359T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.8e-09;
RESULT 1029
ID AAU99036 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S252N/T254S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.8e-09;
RESULT 1030
ID AAU99045 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant Y302N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.8e-09;
RESULT 1031
ID AAU99034 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K251N/T253S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.8e-09;
RESULT 1032
ID ADM77506 standard; protein; 461 AA.
DE Human protein C variant #4 amino acid sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 9.6e-09;
RESULT 1033
ID AAE08628 standard; protein; 419 AA.
DE Human Protein C derivative #2.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.

Query Match 7.8%; Score 308; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 9.4e-09;
RESULT 1034
ID AAU99084 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R352N/D354T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.6%; Pred. No. 1e-08;
RESULT 1035
ID AAU99021 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K217N/L219S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1e-08;
RESULT 1036
ID AAU99046 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant Y302N/S304T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 1e-08;
RESULT 1037
ID AAU99093 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H388N/Y390S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 1e-08;
RESULT 1038
ID AAU99083 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R352N/D354S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 306.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 1.1e-08;
RESULT 1039
ID AAU99074 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V339T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 306.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.1e-08;
RESULT 1040
ID AAU99003 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D172N/K174S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 306.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.1e-08;
RESULT 1041
ID AEA44152 standard; protein; 419 AA.
DE Human protein C analog with N13K substitution.
PN W02006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 306.5; DB 10; Length 419;
Best Local Similarity 24.1%; Pred. No. 1.1e-08;

RESULT 1042
ID AAR13585 standard; protein; 461 AA.
DE Human protein C zymogen Q313.
PN EP443874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 306.5; DB 2; Length 461;
Best Local Similarity 24.1%; Pred. No. 1.2e-08;
RESULT 1043
ID AAM83654 standard; protein; 495 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3903.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.8%; Score 306.5; DB 8; Length 495;
Best Local Similarity 24.8%; Pred. No. 1.3e-08;
RESULT 1044
ID AED96686 standard; protein; 495 AA.
DE Human C-reactive protein (CRP) associated marker SEQ ID NO 868.
PN W02005107364-A2.
PD 17-NOV-2005.
PA (COMP-) COMPUEN LTD.
PA (COHE/) COHEN Y.
Query Match 7.8%; Score 306.5; DB 9; Length 495;
Best Local Similarity 24.8%; Pred. No. 1.3e-08;
RESULT 1045
ID AAU99004 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D172N/K174T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.7%; Score 305.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.3e-08;
RESULT 1046
ID AAU99073 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V339S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.7%; Score 305.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.3e-08;
RESULT 1047
ID AEA44150 standard; protein; 419 AA.
DE Human protein C analog with Q32M substitution.
PN W02006044294-A2.
PD 27-APR-2006.
PA (ELIL) LILLY & CO ELI.
Query Match 7.7%; Score 305.5; DB 10; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.3e-08;
RESULT 1048
ID AEA20109 standard; protein; 667 AA.
DE Novel human polypeptide SEQ ID NO 803.
PN W02005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 7.7%; Score 305; DB 9; Length 667;
Best Local Similarity 20.8%; Pred. No. 2.1e-08;
RESULT 1049
ID AEG02812 standard; protein; 419 AA.
DE Mature Protein C polypeptide.
PN W02006018204-A1.
PD 23-FEB-2006.
PA (ZLBB-) ZLB BEHRING GMBH.
Query Match 7.7%; Score 304.5; DB 10; Length 419;
Best Local Similarity 24.9%; Pred. No. 1.4e-08;
RESULT 1050
ID AAR13582 standard; protein; 461 AA.
DE Human protein C zymogen Q097.
PN EP443874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.

Query Match 7.7%; Score 304.5; DB 2; Length 461;
Best Local Similarity 24.4%; Pred. No. 1.6e-08;
RESULT 1051
ID AAR13584 standard; protein; 461 AA.
DE Human protein C zymogen Q248.
PN EP43874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.7%; Score 304.5; DB 2; Length 461;
Best Local Similarity 24.4%; Pred. No. 1.6e-08;
RESULT 1052
ID AAU99037 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T253N/D255S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.7%; Score 302.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.9e-08;
RESULT 1053
ID AAU99028 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V243N/V245T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.7%; Score 302.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 1.9e-08;
RESULT 1054
ID AAU99027 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V243N/V245S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 301.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.1e-08;
RESULT 1055
ID AAU99038 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T253N/D255T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 301.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 2.1e-08;
RESULT 1056
ID AAP93714 standard; protein; 461 AA.
DE Hybrid protein of protein-C and Factor-X.
PN EP296413-A.
PD 28-DEC-1988.
PA (FARK) HOECHST JAPAN LTD.
Query Match 7.6%; Score 301.5; DB 1; Length 461;
Best Local Similarity 24.7%; Pred. No. 2.3e-08;
RESULT 1057
ID ADX39098 standard; protein; 681 AA.
DE Mouse factor VII mutant.
PN W02005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 301.5; DB 9; Length 681;
Best Local Similarity 22.3%; Pred. No. 3.3e-08;
RESULT 1058
ID ADX39094 standard; protein; 446 AA.
DE Mouse factor VII.
PN W02005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 300.5; DB 9; Length 446;
Best Local Similarity 22.3%; Pred. No. 2.5e-08;
RESULT 1059
ID AAU99041 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D255N/D257S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 299.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 2.7e-08;
RESULT 1060
ID ADX39097 standard; protein; 443 AA.
DE Rabbit factor VII.
PN W02005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 299.5; DB 9; Length 443;
Best Local Similarity 24.0%; Pred. No. 2.8e-08;
RESULT 1061
ID AAU99029 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V245N/P247S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 298.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 3e-08;
RESULT 1062
ID AAU99030 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V245N/P247T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 298.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 3e-08;
RESULT 1063
ID AAU99042 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D255N/D257T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 298.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 3e-08;
RESULT 1064
ID ADX39092 standard; protein; 433 AA.
DE Danio factor VII.
PN W02005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 298.5; DB 9; Length 433;
Best Local Similarity 23.0%; Pred. No. 3.1e-08;
RESULT 1065
ID ADB65750 standard; protein; 397 AA.
DE Human protein encoded by clone UTERU20087070.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HEIL-) HELIX RES INST.
Query Match 7.6%; Score 298; DB 7; Length 397;
Best Local Similarity 24.1%; Pred. No. 3.1e-08;
RESULT 1066
ID AEL57571 standard; protein; 543 AA.
DE Human t-Plasminogen activator precursor, SEQ ID NO: 2034.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS/) BETSHOLTZ C.
PA (TRYG/) TRYGVASON K.
PA (TRAK/) TAKEMOTO M.
PA (HEIL/) HE L.
PA (PATR/) PATRAKAS J.
Query Match 7.5%; Score 297.5; DB 10; Length 543;
Best Local Similarity 23.0%; Pred. No. 4.4e-08;
RESULT 1067
ID ADL1268 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SegID 804.

PN W0200268649-A2.
PA (CURA-) CURAGEN CORP.
Query Match 7.5%; Score 296; DB 5; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.4e-08;
RESULT 1068
ID AD117276 standard; protein; 230 AA.
DE Polypeptide homologue to a human NOVX domain Segid 812.
PN W0200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.5%; Score 296; DB 5; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.4e-08;
RESULT 1069
ID ADJ83075 standard; protein; 230 AA.
DE Trypsin-like serine protease protein - SEQ ID 66.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBOOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATY/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILF/) LI L.
PA (CASW/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOULI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 7.5%; Score 296; DB 7; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.4e-08;
RESULT 1070
ID AEF27705 standard; protein; 230 AA.
DE Trypsin-like serine protease consensus sequence, SEQ.135.
PN US2006009634-A1.
PD 12-JAN-2006.
PA (KEKU/) KEKUDA R.
PA (ALSO/) ALSOBOOK J.
PA (TCHE/) TCHERNEV V.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K.
PA (PATY/) PATTURAJAN M.
PA (GROS/) GROSSE W.
PA (LEPL/) LEPLEY D.
PA (BURG/) BURGESS C.
PA (VERN/) VERNET C.
PA (LILF/) LI L.
PA (GORM/) GORMAN L.
PA (EDIN/) EDINGER S.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U.
PA (ROTH/) ROTHENBERG M.
PA (STON/) STONE D.
PA (BOLD/) BOLDOG F.
PA (GROS/) GROSSE W.
PA (SHEN/) SHENOY S.
PA (ANDE/) ANDERSON D.

PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R.
PA (MILL/) MILLER C.
PA (EISE/) EISEN A.
Query Match 7.5%; Score 296; DB 10; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.4e-08;
RESULT 1071
ID AEG02859 standard; protein; 451 AA.
DE Factor VII/X fusion protein SEQ ID NO:53.
PN W02006018204-A1.
PD 23-FEB-2006.
PA (ZLIB-) ZLB BEHRING GMBH.
Query Match 7.5%; Score 296; DB 10; Length 451;
Best Local Similarity 25.2%; Pred. No. 4.4e-08;
RESULT 1072
ID ADM64351 standard; protein; 527 AA.
DE Mutant human plasminogen activator protein - SEQ ID 3.
PN CN1526726-A.
PD 08-SEP-2004.
PA (LIBB/) LI B.
Query Match 7.5%; Score 296; DB 8; Length 527;
Best Local Similarity 23.4%; Pred. No. 5.1e-08;
RESULT 1073
ID ABG21442 standard; protein; 932 AA.
DE Novel human diagnostic protein #21433.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.5%; Score 296; DB 4; Length 932;
Best Local Similarity 21.0%; Pred. No. 8.8e-08;
RESULT 1074
ID ADX39096 standard; protein; 425 AA.
DE Chicken factor VII.
PN W02005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.5%; Score 295; DB 9; Length 425;
Best Local Similarity 23.4%; Pred. No. 4.8e-08;
RESULT 1075
ID AAR09290 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue Gr6 (Ieu 66, Asp 67, Thr 68, Gln 117).
PN W08912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match 7.5%; Score 294; DB 2; Length 562;
Best Local Similarity 23.3%; Pred. No. 7e-08;
RESULT 1076
ID ADX39099 standard; protein; 407 AA.
DE Bovine factor VII.
PN W02005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.4%; Score 293.5; DB 9; Length 407;
Best Local Similarity 24.1%; Pred. No. 5.5e-08;
RESULT 1077
ID ABU12065 standard; protein; 986 AA.
DE Human NOV12a CG92293-01 protein SEQ ID 50.
PN W0200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.4%; Score 293; DB 6; Length 986;
Best Local Similarity 21.8%; Pred. No. 1.3e-07;
RESULT 1078
ID AAR70903 standard; protein; 527 AA.
DE Human c-PA variant (N103,A432,A434).
PN US5385732-A.
PD 31-JAN-1995.
PA (GENTH) GENENTECH INC.
Query Match 7.4%; Score 292; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 8.4e-08;
RESULT 1079
ID AAR70895 standard; protein; 527 AA.

DE Human t-PA variant (N103,A331,A332).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 292; DB 2; Length 527;
RESULT 1080
ID ADN03787 standard; protein; 516 AA.
DE Antisporiatric protein sequence #90.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 291.5; DB 8; Length 516;
RESULT 1081
ID ABM80985 standard; protein; 516 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81669, SEQ:2539.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 291.5; DB 8; Length 516;
RESULT 1082
ID ADQ3246 standard; protein; 516 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 909.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPIERA CORP.
Query Match
Best Local Similarity 7.4%; Score 291.5; DB 8; Length 516;
RESULT 1083
ID AEL57575 standard; protein; 516 AA.
DE Human t-plasminogen activator precursor, SEQ ID NO: 2038.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS/) BETSHOLTZ C.
PA (TRYG/) TRYGVASON K.
PA (TAKE/) TAKEMOTO M.
PA (HELL/) HE L.
PA (PATR/) PATRAKAS J.
Query Match
Best Local Similarity 7.4%; Score 291.5; DB 10; Length 516;
RESULT 1084
ID AAR13921 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with H432A and R434A substns.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 291.5; DB 2; Length 522;
RESULT 1085
ID AAP70475 standard; protein; 564 AA.
DE Sequence of tissue plasminogen (TPA) analogue.
PN WO8703906-A.
PD 02-JUL-1987.
PA (UPJO) UPJOHN CO.
PA (MARO/) MAROTTI K R.
Query Match
Best Local Similarity 7.4%; Score 291.5; DB 1; Length 564;
RESULT 1086
ID ADG8338 standard; protein; 376 AA.
DE Rough scale snake venom prothrombin activator, trocarin.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match
Best Local Similarity 7.4%; Score 291; DB 8; Length 376;
RESULT 1087
ID AAP60614 standard; protein; 516 AA.
DE Plasmid pDAF3 encoded sequence.
PN JP61139386-A.
PD 26-JUN-1986.
PA (TOYJ) TOYO SODA MFG CO LTD.

PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (CENG) CENTRAL GLASS CO LTD.
PA (HODO) HODOGAYA CHEM IND CO LTD.
Query Match
Best Local Similarity 7.4%; Score 290.5; DB 1; Length 516;
RESULT 1088
ID AAP70257 standard; protein; 516 AA.
DE Sequence of human tissue plasminogen activator (TPA) and leader.
PN EP231883-A.
PD 12-AUG-1987.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (NIPS) NIPPON SODA CO.
PA (CENG) CENTRAL GLASS CO LTD.
PA (TOYJ) TOYO SODA MFG CO LTD.
PA (NISC) NISSAN CHEM IND LTD.
PA (NISC) NISSAN CHEMICAL INDS KK.
Query Match
Best Local Similarity 7.4%; Score 290.5; DB 1; Length 516;
RESULT 1089
ID AAR70878 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,D184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 290; DB 2; Length 483;
RESULT 1090
ID AAR70885 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,D184,E275,1277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 290; DB 2; Length 483;
RESULT 1091
ID AAR70894 standard; protein; 527 AA.
DE Human t-PA variant (N103,A303,A304).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 290; DB 2; Length 527;
RESULT 1092
ID ADM64350 standard; protein; 527 AA.
DE Mutant human plasminogen activator protein - SEQ ID 2.
PN CN1526726-A.
PD 08-SEP-2004.
PA (LIBB/) LI B.
Query Match
Best Local Similarity 7.4%; Score 290; DB 8; Length 527;
RESULT 1093
ID ADL00357 standard; protein; 520 AA.
DE Human tissue type plasminogen activator (h-tPA) mutant polypeptide.
PN CN1397564-A.
PD 19-FEB-2003.
PA (LIBB/) LI B.
Query Match
Best Local Similarity 7.3%; Score 289.5; DB 7; Length 520;
RESULT 1094
ID AAR12340 standard; protein; 559 AA.
DE T-PA variant contg. fibrinectin for thrombosis lysis (1).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match
Best Local Similarity 7.3%; Score 289.5; DB 2; Length 559;
RESULT 1095
ID AAR22664 standard; protein; 564 AA.
DE tPA analogue KK2A.
PN US5106741-A.
PD 21-APR-1992.
PA (UPJO) UPJOHN CO.
Query Match
Best Local Similarity 7.3%; Score 289.5; DB 2; Length 564;

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Best Local Similarity 23.4%; Pred. No. 1.2e-07;
RESULT 1096
ID AAE06934 standard; protein; 658 AA.
DE Human membrane-type serine protease (MTSP) 4-S splice variant.
PN W0200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 4; Length 658;
Best Local Similarity 22.7%; Pred. No. 1.4e-07;
RESULT 1097
ID AD110379 standard; protein; 658 AA.
DE Human cell surface protease #5.
PN W0200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 7; Length 658;
Best Local Similarity 22.7%; Pred. No. 1.4e-07;
RESULT 1098
ID ADJ46903 standard; protein; 658 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #5.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 8; Length 658;
Best Local Similarity 22.7%; Pred. No. 1.4e-07;
RESULT 1099
ID AAE06933 standard; protein; 802 AA.
DE Human membrane-type serine protease (MTSP) 4-L splice variant.
PN W0200157194-A2.
PD 03-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 4; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.7e-07;
RESULT 1100
ID AD110377 standard; protein; 802 AA.
DE Human cell surface protease #4.
PN W0200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.7e-07;
RESULT 1101
ID ADJ46901 standard; protein; 802 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #4.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.7e-07;
RESULT 1102
ID AAR21598 standard; protein; 527 AA.
DE cPA variant - T103N, D236A, D238A, K240A.
PN W09202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 289; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.2e-07;
RESULT 1103
ID AAR09217 standard; protein; 529 AA.
DE c-PA insertion variant I304 HH.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 289; DB 2; Length 529;
Best Local Similarity 23.4%; Pred. No. 1.2e-07;
RESULT 1104
ID AAB85076 standard; peptide; 296 AA.
DE Amino acid sequence of MASP-1 polypeptide.
PN W0200140451-A2.
PD 07-JUN-2001.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 7.3%; Score 288.5; DB 4; Length 296;

Best Local Similarity 29.3%; Pred. No. 7.6e-08;
RESULT 1105
ID AAY41710 standard; protein; 802 AA.
DE Human PRO618 protein sequence.
PN W09946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 2; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1106
ID AAB44266 standard; protein; 802 AA.
DE Human PRO618 (UNQ354) protein sequence SEQ ID NO:169.
PN W0200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 3; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1107
ID AAB24052 standard; protein; 802 AA.
DE Human PRO618 protein sequence SEQ ID NO:24.
PN W0200053754-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 3; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1108
ID AAU82755 standard; protein; 802 AA.
DE Amino acid sequence of novel human protease #54.
PN W0200200860-A2.
PD 03-JAN-2002.
PA (SUGE-) SUGEN INC.
Query Match 7.3%; Score 288.5; DB 5; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1109
ID ABO25212 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1110
ID ABU72218 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1111
ID ABU84898 standard; protein; 802 AA.
DE Human secreted and transmembrane polypeptide PRO618.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1112
ID ABU61096 standard; protein; 802 AA.
DE Human PRO618 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1113
ID ABU80365 standard; protein; 802 AA.
DE Human secreted/transmembrane protein PRO618.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
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RESULT 1114
ID ADA24708 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1115
ID ABO19667 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1116
ID ADA12369 standard; protein; 802 AA.
DE Human secreted/transmembrane polypeptide PRO618.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1117
ID ABO19558 standard; protein; 802 AA.
DE Novel human secreted and transmembrane polypeptide #26.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1118
ID ADB73675 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1119
ID ADB76391 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1120
ID ADC43817 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1121
ID ADC61577 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1122
ID ADC63541 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1123
ID ADC66641 standard; protein; 802 AA.

DE Human secreted/transmembrane protein, PRO618.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1124
ID ADC68765 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1125
ID ADC62825 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1126
ID ADC67890 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003068178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1127
ID ADC41210 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1128
ID ADC67265 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1129
ID ADC62201 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1130
ID ADC41834 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1131
ID ADE49203 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1132
ID ADE35257 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.

PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1133
ID ADE16371 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1134
ID ADD72986 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1135
ID ADD72344 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1136
ID ADE16995 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1137
ID ADF47009 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1138
ID ADF3936 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1139
ID ADG60086 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1140
ID ADI60846 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1141
ID ADB48503 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1142
ID ADE89604 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US200310181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANU/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1143
ID ADF61244 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1144
ID ADF3936 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1145
ID ADF45732 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1146
ID ADF24128 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1147
ID ADF40560 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.

PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1148
ID ADF23504 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1149
ID ADF33487 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1150
ID ADF26954 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1151
ID ADF27590 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1152
ID ADF41184 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1153
ID ADF32863 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1154
ID ADF25229 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1155
ID ADF26330 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1156
ID ADF34119 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194410-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1157
ID ADF46356 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1158
ID ADF50342 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1159
ID ADF49718 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1160
ID ADF51590 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1161
ID ADF49094 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1162
ID ADF48470 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1163
ID ADF50966 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1164
ID ADF58910 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1165
ID ADF62366 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004006219-A1.
PD 08-JAN-2004.

PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1166
ID ADH25391 standard; protein; 802 AA.
DE Human neurotrophin homologue related protein sequence SEQ ID NO:169.
PN EP136931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1167
ID ADM17168 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US200404832-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1168
ID ADL07002 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1169
ID ADT91615 standard; protein; 802 AA.
DE Human PRO618 protein sequence.
PN AU2002317529-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1170
ID ADU50124 standard; protein; 802 AA.
DE PRO618, SEQ ID 169.
PN US2004233964-A1.
PD 11-NOV-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1171
ID ADM49403 standard; protein; 802 AA.
DE PRO618 protein, SEQ ID 169.
PN US2005014226-A1.
PD 20-JAN-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATC/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANT/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEM/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 288.5; DB 9; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1172
ID ADZ52064 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2005084935-A1.
PD 21-APR-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATC/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANT/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEM/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 288.5; DB 9; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1173
ID AED47892 standard; protein; 802 AA.
DE Human PRO618 amino acid sequence.
PN US2005227342-A1.
PD 13-OCT-2005.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 9; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1174
ID AEH18123 standard; protein; 802 AA.
DE Human PRO protein amino acid sequence - SEQ ID 169.
PN US2006078964-A1.
PD 13-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 10; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1175
ID AAB98507 standard; protein; 902 AA.
DE Murine epithin.
PN WO200129056-A1.
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.3%; Score 288.5; DB 4; Length 902;
Best Local Similarity 21.4%; Pred. No. 2.2e-07;
RESULT 1176
ID AAU80517 standard; protein; 902 AA.
DE Mouse epithilin-like serine protease.
PN WO200196378-A2.
PD 20-DEC-2001.
PA (FARB) BAYER AG.
Query Match 7.3%; Score 288.5; DB 5; Length 902;
Best Local Similarity 21.4%; Pred. No. 2.2e-07;
RESULT 1177
ID AAU77549 standard; protein; 902 AA.
DE Murine type II membrane serine protease, epithin.

PN W0200212461-A2.
PD 14-FEB-2002.
PA (FARB) BAYER AG.
Query Match 7.3%; Score 288.5; DB 5; Length 902;
Best Local Similarity 21.4%; Pred. No. 2.2e-07;
RESULT 1178
ID AAR05489 standard; protein; 527 AA.
DE tPA024 precursor protein.
PN E8373896-A.
PD 20-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
PA (YAMA) NIPPON STEEL CORP.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.6%; Pred. No. 1.4e-07;
RESULT 1179
ID AAR21599 standard; protein; 527 AA.
DE tPA variant - N117Q, D236A, D238A, K240A.
PN W09202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1180
ID AAR20220 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-012.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
RESULT 1181
ID AAR20219 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-011.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
RESULT 1182
ID AAR20217 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-009.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
RESULT 1183
ID AAR20218 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-010.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
RESULT 1184
ID AAR70901 standard; protein; 527 AA.
DE Human t-PA variant (N103,A416,A417,A418).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 1.4e-07;
RESULT 1185
ID AAR70904 standard; protein; 527 AA.
DE Human t-PA variant (N103,A440).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1186
ID AAY9558 standard; protein; 356 AA.
DE Human protein C protein sequence.

PN W09950454-A2.
PD 07-OCT-1999.
PA (WHEE) WHITEHEAD INST BIOMEDICAL RES.
Query Match 7.3%; Score 287.5; DB 2; Length 356;
Best Local Similarity 24.5%; Pred. No. 1e-07;
RESULT 1187
ID AAM52187 standard; protein; 406 AA.
DE Human FVII mutant K143N/N145T/R315N/V317T.
PN W0200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.3%; Score 287.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1188
ID ADU56078 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K143N/ N145T/ R290N/ A292T.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 287.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1189
ID ADV44720 standard; protein; 406 AA.
DE Human factor VII mutant K143N/N145T/R315N/V317T.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 287.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1190
ID ADV74310 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #253.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 287.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1191
ID AEF15066 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #35.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 287.5; DB 10; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1192
ID AAR13918 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with K116A, H417A and E418A substns.
PN W09113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287.5; DB 2; Length 522;
Best Local Similarity 22.9%; Pred. No. 1.5e-07;
RESULT 1193
ID ABP43952 standard; protein; 795 AA.
DE Human PRO618.
PN W0200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 7.3%; Score 287.5; DB 5; Length 795;
Best Local Similarity 22.7%; Pred. No. 2.2e-07;
RESULT 1194
ID ADG83828 standard; protein; 467 AA.
DE Coastal taipan venom protease.
PN W02003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match 7.3%; Score 287; DB 8; Length 467;
Best Local Similarity 22.5%; Pred. No. 1.4e-07;
RESULT 1195
ID AAR70879 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,S184,E275).
PN US5385732-A.

PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1196
ID AAR70883 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K210,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1197
ID AAR70884 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1198
ID AAR70886 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,S184,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1199
ID AAR70877 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1200
ID AAR70887 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K213,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1201
ID AAR70881 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R210,A211,R212,R213,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1202
ID AAR70882 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R252,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1203
ID AAR70889 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R252,E275,O277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1204
ID AAR70888 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R210,A211,R212,R213,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.

PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 1.4e-07;
RESULT 1205
ID AAR70890 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K210,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1206
ID AAR70880 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K213,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1207
ID AAR70907 standard; protein; 527 AA.
DE Human t-PA variant (N103,A460,A462) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.6e-07;
RESULT 1208
ID AAR70874 standard; protein; 527 AA.
DE Human t-PA variant (N67,N103) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.6e-07;
RESULT 1209
ID AAR70892 standard; protein; 527 AA.
DE Human t-PA variant (N103,A283,A287) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.6e-07;
RESULT 1210
ID AAM52182 standard; protein; 406 AA.
DE Human FVII mutant K143N/N145T.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.3%; Score 286.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.3e-07;
RESULT 1211
ID ADU56073 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K143N/N145T.
PN WO200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.3e-07;
RESULT 1212
ID AD010589 standard; protein; 406 AA.
DE Human factor VII/VIII protein mutant #25.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.3e-07;
RESULT 1213
ID ADV44715 standard; protein; 406 AA.
DE Human factor VII mutant K143N/N145T.
PN WO2004110469-A2.
PD 23-DEC-2004.

PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 286.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.3e-07;
RESULT 1214
ID ADY74305 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #248.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 286.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.3e-07;
RESULT 1215
ID AEF15046 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #15.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 286.5; DB 10; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.3e-07;
RESULT 1216
ID ADG83826 standard; protein; 467 AA.
DE Brown snake venom protease.
PN W02003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match 7.3%; Score 286.5; DB 8; Length 467;
Best Local Similarity 22.2%; Pred. No. 1.5e-07;
RESULT 1217
ID AAR14486 standard; protein; 522 AA.
DE Delta (466-470) CPA variant with Y67N substitution.
PN W09113149-A.
PD 05-SEP-1991.
PA (GENTH) GENTENTECH INC.
Query Match 7.3%; Score 286.5; DB 2; Length 522;
Best Local Similarity 22.7%; Pred. No. 1.7e-07;
RESULT 1218
ID AAR44816 standard; protein; 527 AA.
DE Human CPA variant (N67,N103).
PN US5270198-A.
PD 14-DEC-1993.
PA (GENTH) GENTENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.8e-07;
RESULT 1219
ID AAR44812 standard; protein; 527 AA.
DE Human CPA variant N103.
PN US5270198-A.
PD 14-DEC-1993.
PA (GENTH) GENTENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.8e-07;
RESULT 1220
ID AAR70868 standard; protein; 527 AA.
DE Human t-PA variant (N67,A432,A434).
PN US5385732-A.
PD 31-JAN-1995.
PA (GENTH) GENTENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.8e-07;
RESULT 1221
ID AAR70860 standard; protein; 527 AA.
DE Human t-PA variant (N67,A331,A332).
PN US5385732-A.
PD 31-JAN-1995.
PA (GENTH) GENTENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.8e-07;
RESULT 1222
ID AAR70900 standard; protein; 527 AA.
DE Human t-PA variant (N103,A410).
PN US5385732-A.
PD 31-JAN-1995.
PA (GENTH) GENTENTECH INC.

Query Match 7.2%; Score 285; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 1.8e-07;
RESULT 1223
ID AAR09220 standard; protein; 529 AA.
DE t-PA insertion variant 1304H, 1305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENTH) GENTENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 529;
Best Local Similarity 23.2%; Pred. No. 1.8e-07;
RESULT 1224
ID AAP70449 standard; protein; 530 AA.
DE Sequence encoded by of synthetic gene for mature human tissue plasminogen activator (tPA).
PN W08705934-A.
PD 08-OCT-1987.
PA (CREA/) CREA R.
Query Match 7.2%; Score 286; DB 1; Length 530;
Best Local Similarity 22.9%; Pred. No. 1.8e-07;
RESULT 1225
ID AAR12342 standard; protein; 561 AA.
DE T-PA with -ve charged finger and/or kringle domain (1).
PN JF03061483-A.
PD 18-MAR-1991.
PA (FUJISAWA PHARM CO LTD).
Query Match 7.2%; Score 286; DB 2; Length 561;
Best Local Similarity 22.1%; Pred. No. 1.9e-07;
RESULT 1226
ID AAR09289 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT12 (Asp 67, Thr 68).
PN W08912681-A.
PD 28-DEC-1989.
PA (BRRI-) BRIT BIO-TECHN LTD.
Query Match 7.2%; Score 286; DB 2; Length 562;
Best Local Similarity 23.3%; Pred. No. 1.9e-07;
RESULT 1227
ID AAP70880 standard; protein; 527 AA.
DE Thrombolytic proteins 1-9-1-11 having t-PA activity and R275 is deleted or replaced and containing a modified N-linked glycosylation site.
PN W08704722-A.
PD 13-AUG-1987.
PA (GEMV) GENETICS INST INC.
PA (LARS/) LARSEN G R.
Query Match 7.2%; Score 285.5; DB 1; Length 527;
Best Local Similarity 23.1%; Pred. No. 1.9e-07;
RESULT 1228
ID AAP91683 standard; protein; 527 AA.
DE Sequence of tissue plasminogen activator (tPA).
PN W08911531-A.
PD 30-NOV-1989.
PA (GENTH) GENTENTECH INC.
Query Match 7.2%; Score 285; DB 1; Length 527;
Best Local Similarity 23.2%; Pred. No. 2e-07;
RESULT 1229
ID AAR09270 standard; protein; 527 AA.
DE t-PA variant H331A, H332A.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENTH) GENTENTECH INC.
Query Match 7.2%; Score 285; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2e-07;
RESULT 1230
ID AAR09278 standard; protein; 527 AA.
DE t-PA variant H432A, R434A.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENTH) GENTENTECH INC.
Query Match 7.2%; Score 285; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2e-07;
RESULT 1231
ID ADW64349 standard; protein; 527 AA.
DE Mutant human plasminogen activator protein - SEQ ID 1.

PN CN1526726-A.
PD 08-SEP-2004.
PA (LIBA/) LI B.
Query Match 7.2%; Score 285; DB 8; Length 527;
Best Local Similarity 23.0%; Pred. No. 2e-07;
RESULT 1232
ID AAF71449 standard; protein; 528 AA.
DE Modified human tissue plasminogen activator.
PN EP238304-A.
PD 23-SEP-1987.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 1; Length 528;
Best Local Similarity 23.4%; Pred. No. 2e-07;
RESULT 1233
ID AAR13148 standard; protein; 556 AA.
DE T-PA variant contg. fibrinectin for thrombosis lysis (2).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 285; DB 2; Length 556;
Best Local Similarity 21.9%; Pred. No. 2.1e-07;
RESULT 1234
ID AAB1710 standard; protein; 264 AA.
DE Human serine protease BSSP5 (HBSSP5) SEQ ID NO:2.
PN WO200031243-A1.
PD 02-JUN-2000.
PA (FUJO) FUJO PHARM IND LTD.
Query Match 7.2%; Score 284.5; DB 3; Length 264;
Best Local Similarity 28.0%; Pred. No. 1.1e-07;
RESULT 1235
ID AAF91961 standard; protein; 518 AA.
DE Sequence of des 1-44E275 t-PA mutant.
PN WO8909266-A.
PD 05-OCT-1989.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284.5; DB 1; Length 518;
Best Local Similarity 22.9%; Pred. No. 2.1e-07;
RESULT 1236
ID AAM84749 standard; protein; 629 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4998.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY) INCYTE CORP.
Query Match 7.2%; Score 284.5; DB 8; Length 629;
Best Local Similarity 19.5%; Pred. No. 2.5e-07;
RESULT 1237
ID AAM82817 standard; protein; 629 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3066.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY) INCYTE CORP.
Query Match 7.2%; Score 284.5; DB 8; Length 629;
Best Local Similarity 19.5%; Pred. No. 2.5e-07;
RESULT 1238
ID AAR70851 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,D184,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 2.1e-07;
RESULT 1239
ID AAR70844 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,D184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 2.1e-07;
RESULT 1240
ID AAR44809 standard; protein; 527 AA.
DE Human tPA variant (N65, S67).
PN US5270198-A.

PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 2.3e-07;
RESULT 1241
ID AAR70908 standard; protein; 527 AA.
DE Human t-PA variant (N103,A477).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.3e-07;
RESULT 1242
ID AAR70859 standard; protein; 527 AA.
DE Human t-PA variant (N67,A303,A304).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.8%; Pred. No. 2.3e-07;
RESULT 1243
ID AAR70893 standard; protein; 527 AA.
DE Human t-PA variant (N103,A296,A297,A298,A299).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 2.3e-07;
RESULT 1244
ID AAR70891 standard; protein; 527 AA.
DE Human t-PA variant (N103,A267).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.7%; Pred. No. 2.3e-07;
RESULT 1245
ID AAF70474 standard; protein; 562 AA.
DE Sequence of tissue plasminogen (TPA) analogue.
PN WO8703906-A.
PD 02-JUL-1987.
PA (UPJO) UPJOHN CO.
PA (MARCO/) MAROTTI K R.
Query Match 7.2%; Score 284; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 2.4e-07;
RESULT 1246
ID AAR09286 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBRNTS (Ser 67, Ser 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BBRI-) BRIT BIO-TECHN LTD.
Query Match 7.2%; Score 284; DB 2; Length 562;
Best Local Similarity 23.1%; Pred. No. 2.4e-07;
RESULT 1247
ID AAR23807 standard; protein; 562 AA.
DE t-PA (Tyr 297) mutant.
PN WO2006203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.2%; Score 284; DB 2; Length 562;
Best Local Similarity 23.2%; Pred. No. 2.4e-07;
RESULT 1248
ID AAB80068 standard; protein; 406 AA.
DE Human coagulation factor VII mutant L305V/M306D/D309S.
PN WO200183725-A1.
PD 08-NOV-2001.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 5; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1249
ID AAG73125 standard; protein; 406 AA.
DE Human coagulation Factor VII mutant polypeptide L305V/M306D/D309S.
PN WO20027218-A1.

PD 03-OCT-2002.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 6; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1250
ID ADJ55852 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant L305V/ M306D/ D309S.
PN MO2004000386-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 8; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1251
ID ADV44489 standard; protein; 406 AA.
DE Human factor VII mutant L305V/M306D/D309S.
PN MO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 9; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1252
ID ADY74078 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #21.
PN MO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.2%; Score 283.5; DB 9; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.9e-07;
RESULT 1253
ID ADE83543 standard; protein; 482 AA.
DE Rat protein NP 058839, SEQ ID NO 11161.
PN MO2003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.2%; Score 283.5; DB 7; Length 482;
Best Local Similarity 22.8%; Pred. No. 2.2e-07;
RESULT 1254
ID AAR13917 standard; peptide; 522 AA.
DE Delta (466-470) tPA variant with K296A, H297A, R298A and R299A substitutions.
PN MO9113149-A.
PD 05-SEP-1991.
PA (GENE) GENENTECH INC.
Query Match 7.2%; Score 283.5; DB 2; Length 522;
Best Local Similarity 22.8%; Pred. No. 2.4e-07;
RESULT 1255
ID AAP90169 standard; peptide; 571 AA.
DE Tissue plasminogen activator mutant 2G.
PN MO8907146-A.
PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Query Match 7.2%; Score 283.5; DB 1; Length 571;
Best Local Similarity 22.4%; Pred. No. 2.6e-07;
RESULT 1256
ID ADM20190 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #28.
PN MO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.2%; Score 283; DB 9; Length 407;
Best Local Similarity 22.2%; Pred. No. 2e-07;
RESULT 1257
ID AAR09257 standard; protein; 483 AA.
DE t-PA variant dl-44, N184D, I210R, G211A, K212R, V213R, T252R, F305H.
PN MO9002798-A.
PD 22-MAR-1990.
PA (GENE) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.4e-07;
RESULT 1258
ID AAR09269 standard; protein; 527 AA.

DE t-PA variant E303A, R304A.
PN MO9002798-A.
PD 22-MAR-1990.
PA (GENE) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.7%; Pred. No. 2.6e-07;
RESULT 1259
ID AAR44810 standard; protein; 527 AA.
DE Human tPA variant (N65, T67).
PN US5270198-A.
PD 14-DEC-1993.
PA (GENE) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 2.6e-07;
RESULT 1260
ID AAR44817 standard; protein; 527 AA.
DE Human tPA variant (N67, A296, A297, A298, A299).
PN US5270198-A.
PD 14-DEC-1993.
PA (GENE) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.6e-07;
RESULT 1261
ID AAR44814 standard; protein; 527 AA.
DE Human tPA variant (N105, T107).
PN US5270198-A.
PD 14-DEC-1993.
PA (GENE) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.6%; Pred. No. 2.6e-07;
RESULT 1262
ID AAR70899 standard; protein; 527 AA.
DE Human t-PA variant (N103, A408).
PN US5385732-A.
PD 31-JAN-1995.
PA (GENE) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 22.9%; Pred. No. 2.6e-07;
RESULT 1263
ID AAR13341 standard; protein; 560 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (3).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 283; DB 2; Length 560;
Best Local Similarity 22.1%; Pred. No. 2.7e-07;
RESULT 1264
ID AAR13367 standard; protein; 561 AA.
DE T-PA with -ve charged finger and/or kringle domain (7).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 283; DB 2; Length 561;
Best Local Similarity 22.1%; Pred. No. 2.7e-07;
RESULT 1265
ID ADM42867 standard; protein; 925 AA.
DE Human corin protein deletion region 569-1042.
PN MO2004111225-A1.
PD 23-DEC-2004.
PA (SCHD) SCHERING AG.
Query Match 7.2%; Score 283; DB 9; Length 925;
Best Local Similarity 20.5%; Pred. No. 4.4e-07;
RESULT 1266
ID AEG02852 standard; protein; 436 AA.
DE Factor VII/IX fusion protein SEQ ID NO:46.
PN MO2006018204-A1.
PD 23-FEB-2006.
PA (ZLBB-) ZLB BEHRING GMBH.
Query Match 7.2%; Score 282.5; DB 10; Length 436;
Best Local Similarity 24.2%; Pred. No. 2.3e-07;
RESULT 1267
ID ARG02835 standard; peptide; 436 AA.
DE Factor VII/IX fusion protein SEQ ID NO:29.

PN W02006018204-A1.
PD 23-FEB-2006.
PA (ZLBB-) ZLB BEHRING GMBH.
Query Match 7.2%; Score 282.5; DB 10; Length 436;
Best Local Similarity 24.2%; Pred. No. 2.3e-07;
RESULT 1268
ID AAR09231 standard; protein; 524 AA.
DE t-PA deletion variant d297-299.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 282.5; DB 2; Length 524;
Best Local Similarity 22.8%; Pred. No. 2.7e-07;
RESULT 1269
ID ADM20177 standard; protein; 406 AA.
DE Human factor VII (FVII) protein variant sequence #15.
PN W02004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 282; DB 9; Length 406;
Best Local Similarity 22.1%; Pred. No. 2.3e-07;
RESULT 1270
ID ABL92410 standard; protein; 406 AA.
DE Human factor VII protein variant, P10D.
PN W02006114105-A2.
PD 02-NOV-2006.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 282; DB 10; Length 406;
Best Local Similarity 22.3%; Pred. No. 2.3e-07;
RESULT 1271
ID AAR09246 standard; protein; 483 AA.
DE t-PA variant d1-44, N184D, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 2.7e-07;
RESULT 1272
ID AAR09254 standard; protein; 483 AA.
DE t-PA variant d1-44, I210R, G211H, K212Q, V213K, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 483;
Best Local Similarity 22.8%; Pred. No. 2.7e-07;
RESULT 1273
ID AAR09230 standard; protein; 525 AA.
DE t-PA deletion variant d297-298.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 525;
Best Local Similarity 23.4%; Pred. No. 2.9e-07;
RESULT 1274
ID AAR09255 standard; protein; 527 AA.
DE t-PA variant I210R, G211H, K212Q, V213K, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 22.8%; Pred. No. 2.9e-07;
RESULT 1275
ID AAR21600 standard; protein; 527 AA.
DE t-PA variant - E94A, D95A, T103N.
PN W09202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.9e-07;
RESULT 1276
ID AAR70866 standard; protein; 527 AA.
DE Human t-PA variant (N67, A416, A417, A418).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.9e-07;
RESULT 1277
ID AAR70902 standard; protein; 527 AA.
DE Human t-PA variant (N103, A426, A427, A429, A430).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.9e-07;
RESULT 1278
ID AAR70869 standard; protein; 527 AA.
DE Human t-PA variant (N67, A440).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.9e-07;
RESULT 1279
ID AAR82582 standard; protein; 562 AA.
DE tissue plasminogen activator with S-119 subseq for M and QG196-98 subseq
DE for NGT.
PN JP63230083-A.
PD 26-SEP-1988.
PA (EISA) EISAI CO LTD.
Query Match 7.1%; Score 282; DB 1; Length 562;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1280
ID AAR09287 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT6 (Thr 67, Asp 68).
PN W08912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match 7.1%; Score 282; DB 2; Length 562;
Best Local Similarity 23.1%; Pred. No. 3.1e-07;
RESULT 1281
ID AAR23808 standard; protein; 562 AA.
DE t-PA (Glu 298) mutant.
PN W09206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 282; DB 2; Length 562;
Best Local Similarity 23.5%; Pred. No. 3.1e-07;
RESULT 1282
ID AAR23810 standard; protein; 562 AA.
DE t-PA (Gly 301) mutant.
PN W09206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 282; DB 2; Length 562;
Best Local Similarity 23.6%; Pred. No. 3.1e-07;
RESULT 1283
ID AAB84869 standard; protein; 406 AA.
DE Mutant blood coagulant factor VII (FVII-30).
PN JP2001061479-A.
PD 13-MAR-2001.
PA (KAGA) ZH KAGAKU & KESSEI RYOH KENKYUSHO.
Query Match 7.1%; Score 281.5; DB 4; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.4e-07;
RESULT 1284
ID AAM52185 standard; protein; 406 AA.
DE Human FVII mutant G291N.
PN W0200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 281.5; DB 4; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.4e-07;
RESULT 1285
ID AAO30584 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158D/K337A/M298Q).

PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1286
ID AAO30626 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1287
ID AAO30582 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1288
ID AAO30616 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1289
ID AAO30572 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1290
ID AAO30628 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158D/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1291
ID ADJ55926 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1292
ID ADJ55927 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1293
ID ADJ55915 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1294
ID ADJ55970 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.

PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1295
ID ADJ56063 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158D/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1296
ID ADJ55959 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1297
ID ADJ56067 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158T/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1298
ID ADJ55971 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1299
ID ADJ56033 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1300
ID ADJ56076 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant G291N.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1301
ID ADO10585 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #21.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.4e-07;
RESULT 1302
ID ADO10626 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #62.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.4e-07;
RESULT 1303
ID ADJ512886 standard; protein; 406 AA.
DE Human factor VII G237L mutant.

PN WO2004083361-A2.
PD 30-SEP-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.4e-07;
RESULT 1304
ID ADV44566 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/V158T/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1305
ID ADV44707 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158D/M298QV/S314E/K337A/L305V.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1306
ID ADV44568 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/V158D/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1307
ID ADV44718 standard; protein; 406 AA.
DE Human factor VII mutant G291N.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.4e-07;
RESULT 1308
ID ADV44610 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158T/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1309
ID ADV44612 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158D/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1310
ID ADV44673 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/M298Q/K337A/S314E.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1311
ID ADV44556 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1312
ID ADV44704 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158T/S314E/M298Q/K337A/L305V.

PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1313
ID ADV44600 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1314
ID ADV74145 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #88.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1315
ID ADV74296 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #239.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1316
ID ADV74155 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #98.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1317
ID ADV74262 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #205.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1318
ID ADV74293 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #236.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1319
ID ADV74189 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #132.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1320
ID ADV74308 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #251.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.4e-07;
RESULT 1321
ID ADV74201 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #144.
PN WO2005024006-A2.

PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1322
ID ADV74157 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #100.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1323
ID ADV74199 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #142.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1324
ID AEF1516 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #85.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1325
ID AEF15122 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #91.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1326
ID AEF15072 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #41.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1327
ID AEF15160 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #129.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1328
ID AEF15083 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #52.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1329
ID AEF15124 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #93.
PN W02005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1330
ID AEF15157 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #126.
PN W02005123916-A2.
PD 29-DEC-2005.

PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1331
ID AAR09233 standard; protein; 522 AA.
DE t-PA deletion variant d297-301.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENENTECH) INC.
Query Match 7.1%; Score 281.5; DB 2; Length 522;
Best Local Similarity 23.4%; Pred. No. 3.1e-07;
RESULT 1332
ID AAR13919 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with E426A, R427A, K423A and E430A substitutions.
PN W09113149-A.
PD 05-SEP-1991.
PA (GENENTECH) INC.
Query Match 7.1%; Score 281.5; DB 2; Length 522;
Best Local Similarity 22.7%; Pred. No. 3.1e-07;
RESULT 1333
ID AAR09239 standard; protein; 524 AA.
DE t-PA deletion variant d300-302.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENENTECH) INC.
Query Match 7.1%; Score 281.5; DB 2; Length 524;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1334
ID AAR12366 standard; protein; 562 AA.
DE T-PA with -ve charged finger and/or kringle domain (5).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281.5; DB 2; Length 562;
Best Local Similarity 21.9%; Pred. No. 3.3e-07;
RESULT 1335
ID ADM20189 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #27.
PN W02004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 281; DB 9; Length 407;
Best Local Similarity 22.2%; Pred. No. 2.6e-07;
RESULT 1336
ID AAR09249 standard; protein; 483 AA.
DE t-PA variant dl-44, I210R, G211A, K212R, V213K, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENENTECH) INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.3%; Pred. No. 3e-07;
RESULT 1337
ID AAR70855 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,S184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GENENTECH) INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 3e-07;
RESULT 1338
ID AAR70845 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,S184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GENENTECH) INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 3e-07;
RESULT 1339
ID AAR70848 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,R252,E275).
PN US5385732-A.

PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. NO. 3e-07;
RESULT 1340
ID AAR70849 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,K210,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. NO. 3e-07;
RESULT 1341
ID AAR70854 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,R252,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. NO. 3e-07;
RESULT 1342
ID AAR70843 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. NO. 3e-07;
RESULT 1343
ID AAR70846 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,K213,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. NO. 3e-07;
RESULT 1344
ID AAR79144 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,S184,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. NO. 3e-07;
RESULT 1345
ID AAR70850 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. NO. 3e-07;
RESULT 1346
ID AAR70852 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,K213,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. NO. 3e-07;
RESULT 1347
ID AAR70847 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,R210,A211,R212,R213,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. NO. 3e-07;
RESULT 1348
ID AAR70853 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,R210,A211,R212,R213,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.

PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. NO. 3e-07;
RESULT 1349
ID AAR60518 standard; protein; 487 AA.
DE Cat16 Factor-Xa.
PN WO9418227-A2.
PD 18-AUG-1994.
PA (DENZ-) DENZYME APS.
Query Match 7.1%; Score 281; DB 2; Length 487;
Best Local Similarity 22.5%; Pred. NO. 3.1e-07;
RESULT 1350
ID AAW76216 standard; protein; 488 AA.
DE Human Factor X protein.
PN WO9838317-A1.
PD 03-SEP-1998.
PA (IMMO) IMMO NO AG.
Query Match 7.1%; Score 281; DB 2; Length 488;
Best Local Similarity 24.0%; Pred. NO. 3.1e-07;
RESULT 1351
ID AAW76217 standard; protein; 488 AA.
DE Human Factor X protein analogue.
PN WO9838317-A1.
PD 03-SEP-1998.
PA (IMMO) IMMO NO AG.
Query Match 7.1%; Score 281; DB 2; Length 488;
Best Local Similarity 22.6%; Pred. NO. 3.1e-07;
RESULT 1352
ID AAW76218 standard; protein; 488 AA.
DE Human Factor X protein.
PN WO9838318-A1.
PD 03-SEP-1998.
PA (IMMO) IMMO NO AG.
Query Match 7.1%; Score 281; DB 2; Length 488;
Best Local Similarity 24.0%; Pred. NO. 3.1e-07;
RESULT 1353
ID AAB70411 standard; protein; 488 AA.
DE Human factor X protein sequence SEQ ID NO:2.
PN WO200110896-A2.
PD 15-FEB-2001.
PA (BAXT) BAXTER AG.
Query Match 7.1%; Score 281; DB 4; Length 488;
Best Local Similarity 24.0%; Pred. NO. 3.1e-07;
RESULT 1354
ID AAR60502 standard; protein; 492 AA.
DE Serine protease for fusion protein cleavage.
PN WO9418227-A2.
PD 18-AUG-1994.
PA (DENZ-) DENZYME APS.
Query Match 7.1%; Score 281; DB 2; Length 492;
Best Local Similarity 22.5%; Pred. NO. 3.1e-07;
RESULT 1355
ID AAR09238 standard; protein; 525 AA.
DE t-PA deletion variant d300-301.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 525;
Best Local Similarity 22.8%; Pred. NO. 3.3e-07;
RESULT 1356
ID AAR09276 standard; protein; 527 AA.
DE t-PA variant K416A, H417A, E418A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. NO. 3.3e-07;
RESULT 1357
ID AAR09279 standard; protein; 527 AA.
DE t-PA variant R440A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.

Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1358
ID AAR70875 standard; protein; 527 AA.
DE Human t-PA variant (N60,N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1359
ID AAR70876 standard; protein; 527 AA.
DE Human t-PA variant (N60,N67,N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1360
ID AAR70857 standard; protein; 527 AA.
DE Human t-PA variant (N67,A283,A287).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1361
ID AAR70898 standard; protein; 527 AA.
DE Human t-PA variant (N103,A364,A365,A366).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1362
ID AAR70906 standard; protein; 527 AA.
DE Human t-PA variant (N103,A449,A453).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1363
ID AAR70872 standard; protein; 527 AA.
DE Human t-PA variant (N67,A460,A462).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1364
ID AAR70842 standard; protein; 527 AA.
DE Wild type tissue plasminogen activator protein.
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1365
ID AAR13150 standard; protein; 558 AA.
DE T-PA with -ve charged finger and/or kringle domain (3).
PN JF03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281; DB 2; Length 558;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1366
ID AAR13152 standard; protein; 559 AA.
DE T-PA with -ve charged finger and/or kringle domain (6).
PN JF03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281; DB 2; Length 559;

Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1367
ID AAR80691 standard; protein; 1087 AA.
DE Hybrid plasminogen/t-PA compound 1.
PN EP292326-A.
PD 23-NOV-1988.
PA (BEECH) BEECHAM GROUP PLC.
Query Match 7.1%; Score 281; DB 1; Length 1087;
Best Local Similarity 22.3%; Pred. No. 6.5e-07;
RESULT 1368
ID ABM81778 standard; protein; 264 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ:4580.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280.5; DB 8; Length 264;
Best Local Similarity 27.2%; Pred. No. 1.8e-07;
RESULT 1369
ID ABM64054 standard; protein; 279 AA.
DE Human diagnostic and therapeutic protease ID NO:4303.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY) INCYTE CORP.
Query Match 7.1%; Score 280.5; DB 8; Length 279;
Best Local Similarity 27.2%; Pred. No. 1.9e-07;
RESULT 1370
ID AAO30575 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1371
ID AAO30604 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1372
ID AAO30577 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1373
ID AAO30594 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1374
ID AAO30569 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1375
ID AAO30606 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;

RESULT 1376
ID AAO30613 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/M298Q).
PN W0200400366-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1377
ID AAO30621 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T/M298Q).
PN W0200400366-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1378
ID AAO30619 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158D/M298Q).
PN W0200400366-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1379
ID ADJ55676 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant / M298Q/ L305V/ K337A.
PN W0200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1380
ID ADJ55937 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316H/ K337A.
PN W0200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1381
ID ADJ56047 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158D/ M298Q/ L305V/ S314E.
PN W0200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1382
ID ADJ55949 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316H/ K337A.
PN W0200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1383
ID ADJ55965 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316Q.
PN W0200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1384
ID ADJ55948 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316H/ K337A.
PN W0200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1385

ID ADJ56057 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y V158T M298Q L305V S314E.
PN W0200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1386
ID ADJ55885 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K337A.
PN W0200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1387
ID ADJ55921 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E.
PN W0200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1388
ID ADJ55958 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316Q.
PN W0200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1389
ID ADJ55963 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316Q.
PN W0200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1390
ID ADJ56016 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/ M298Q/ S314E.
PN W0200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1391
ID ADJ56046 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158D/ M298Q/ L305V/ K337A.
PN W0200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1392
ID ADJ55919 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ S314E.
PN W0200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1393
ID ADJ56056 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158T/ M298Q/ L305V/ K337A.
PN W0200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1394
ID ADJ55887 standard; protein; 406 AA.

DE Human factor VII polypeptide mutant V158D/M298Q/L305V/K337A.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1395
ID ADV55914 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/L305V/S314E.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1396
ID ADV5604 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/L305V/K337A/M298Q.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1397
ID ADO10616 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #52.
PN W02004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.8e-07;
RESULT 1398
ID ADO10607 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #43.
PN W02004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.8e-07;
RESULT 1399
ID ADV44553 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1400
ID ADV44514 standard; protein; 406 AA.
DE Human factor VII mutant L305V/K337A/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1401
ID ADV44526 standard; protein; 406 AA.
DE Human factor VII mutant L305V/M298Q/K337A/V158D.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1402
ID ADV44588 standard; protein; 406 AA.
DE Human factor VII mutant K316H/L305V/V158T/K337A/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1403

ID ADV44597 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1404
ID ADV44605 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158T/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1405
ID ADV44655 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/M298Q/S314E.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1406
ID ADV44645 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/K337A/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1407
ID ADV44686 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/V158D/S314E/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1408
ID ADV44524 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/V158D/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1409
ID ADV44559 standard; protein; 406 AA.
DE Human factor VII mutant L305V/M298Q/K337A/V158T.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1410
ID ADV44694 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158T/L305V/K337A/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1411
ID ADV44684 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/V158D/K337A/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1412
ID ADV44561 standard; protein; 406 AA.

DE Human factor VII mutant S314E/L305V/V158T/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1413
ID ADV44696 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158T/L305V/S314E/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1414
ID ADV44578 standard; protein; 406 AA.
DE Human factor VII mutant K316H/L305V/K337A/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1415
ID ADV44590 standard; protein; 406 AA.
DE Human factor VII mutant K316H/L305V/V158D/K337A/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1416
ID ADV44603 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158D/M298Q.
PN W02004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1417
ID ADM20180 standard; protein; 406 AA.
DE Human factor VII (FVII) protein variant sequence #18.
PN W02004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.8e-07;
RESULT 1418
ID ADM20183 standard; protein; 406 AA.
DE Human factor VII (FVII) protein variant sequence #21.
PN W02004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.8e-07;
RESULT 1419
ID ADV74113 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #56.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1420
ID ADV74285 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #228.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1421
ID ADV74273 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #85.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1422
ID ADV74150 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #93.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1423
ID ADV74177 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #120.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1424
ID ADV74073 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #16.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.8e-07;
RESULT 1425
ID ADV74148 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #91.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1426
ID ADV74179 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #122.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1427
ID ADV74275 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #218.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1428
ID ADV74283 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #226.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1429
ID ADV74103 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #46.
PN W02005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1430
ID ADV74273 standard; protein; 406 AA.

DE Human Factor VII variant polypeptide #216.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1431
ID ADY74194 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #137.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1432
ID ADY74186 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #129.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1433
ID ADY74192 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #135.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1434
ID ADY74234 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #177.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1435
ID ADY74115 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #58.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1436
ID ADY74244 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #187.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1437
ID ADY74167 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #110.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1438
ID AEF15119 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #88.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1439
ID AEF15089 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #58.

PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1440
ID AEF15073 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #42.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1441
ID AEF15099 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #68.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1442
ID AEF15146 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #115.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1443
ID AEF15136 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #105.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1444
ID AEF15134 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #103.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1445
ID AEF15077 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #46.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1446
ID AEF15086 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #55.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1447
ID AEF15144 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #113.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.8e-07;
RESULT 1448
ID ADM20193 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #31.

PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 407;
Best Local Similarity 22.6%; Pred. No. 2.8e-07;
RESULT 1449
ID AWM20196 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #34.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 407;
Best Local Similarity 22.6%; Pred. No. 2.8e-07;
RESULT 1450
ID AAR09221 standard; protein; 526 AA.
DE t-PA deletion variant d297.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 280.5; DB 2; Length 526;
Best Local Similarity 23.1%; Pred. No. 3.5e-07;
RESULT 1451
ID AAP70020 standard; protein; 561 AA.
DE Sequence of tissue plasminogen activator (tPA).
PN EP242836-A.
PD 28-OCT-1987.
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
Query Match 7.1%; Score 280.5; DB 1; Length 561;
Best Local Similarity 21.7%; Pred. No. 3.7e-07;
RESULT 1452
ID AAR6249 standard; protein; 583 AA.
DE Bovine recombinant prothrombin, expressed in Escherichia coli.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.1%; Score 280.5; DB 7; Length 583;
Best Local Similarity 21.9%; Pred. No. 3.9e-07;
RESULT 1453
ID AAR62451 standard; protein; 635 AA.
DE Bovine recombinant prothrombin, expressed in CHO cells.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.1%; Score 280.5; DB 7; Length 635;
Best Local Similarity 21.9%; Pred. No. 4.2e-07;
RESULT 1454
ID ADM20176 standard; protein; 406 AA.
DE Human factor VII (FVII) protein variant sequence #14.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280; DB 9; Length 406;
Best Local Similarity 22.1%; Pred. No. 2.9e-07;
RESULT 1455
ID AWM20188 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #26.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280; DB 9; Length 407;
Best Local Similarity 22.2%; Pred. No. 2.9e-07;
RESULT 1456
ID AAR37402 standard; protein; 448 AA.
DE Factor X.
PN WO9309803-A1.
PD 27-MAY-1993.
PA (SCHAF) SCHAFER S C.
Query Match 7.1%; Score 280; DB 2; Length 448;
Best Local Similarity 24.0%; Pred. No. 3.2e-07;

RESULT 1457
ID AAM66092 standard; peptide; 448 AA.
DE Human factor X variant.
PN WO9839456-A1.
PD 11-SEP-1998.
PA (UNIW) UNIV WASHINGTON.
Query Match 7.1%; Score 280; DB 2; Length 448;
Best Local Similarity 24.0%; Pred. No. 3.2e-07;
RESULT 1458
ID AEC01740 standard; protein; 490 AA.
DE Modified FVII-UBA-GPI cassette.
PN WO2005073375-A1.
PD 11-AUG-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280; DB 9; Length 490;
Best Local Similarity 22.1%; Pred. No. 3.5e-07;
RESULT 1459
ID AAR09245 standard; protein; 525 AA.
DE t-PA deletion variant d297, d305.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 525;
Best Local Similarity 23.1%; Pred. No. 3.7e-07;
RESULT 1460
ID AAR05488 standard; protein; 527 AA.
DE tPA024 precursor protein.
PN EP373896-A.
PD 20-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1461
ID AAR09267 standard; protein; 527 AA.
DE t-PA variant D283A, H287A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1462
ID AAR09282 standard; protein; 527 AA.
DE t-PA variant D460A, R462A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1463
ID AAR13911 standard; protein; 527 AA.
DE t-PA deriv. (II).
PN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1464
ID AAR13914 standard; protein; 527 AA.
DE t-PA deriv. (V).
PN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1465
ID AAR13912 standard; protein; 527 AA.
DE t-PA deriv. (III).
PN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;

Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1466
ID AAR1310 standard; protein; 527 AA.
DE t-PA deriv. (I).
PN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1467
ID AAR21594 standard; protein; 527 AA.
DE t-PA variant - D95A.
PN MO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1468
ID AAR21593 standard; protein; 527 AA.
DE t-PA variant - E94A.
PN MO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 3.7e-07;
RESULT 1469
ID AAR20221 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM6-013.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1470
ID AAR20215 standard; protein; 527 AA.
DE R462G t-PA analogue.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1471
ID AAR20216 standard; protein; 527 AA.
DE R462G t-PA analogue.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1472
ID AAR20222 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM6-014.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1473
ID AAR20223 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM6-018.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1474
ID AAR44811 standard; protein; 527 AA.
DE Human tPA variant N67.
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;

RESULT 1475
ID AAR70865 standard; protein; 527 AA.
DE Human t-PA variant (N67, A410).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 22.9%; Pred. No. 3.7e-07;
RESULT 1476
ID AAM57778 standard; protein; 527 AA.
DE R275E, H417D human tissue-type plasminogen activator protein mutant.
PN MO9821320-A2.
PD 22-MAY-1998.
PA (SCRI) SCRIPPS RES INST.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1477
ID AAM45907 standard; peptide; 527 AA.
DE Single chain form of the intact t-PA molecule.
PN MO9802454-A2.
PD 22-JAN-1998.
PA (ADPR-) ADPROTECH PLC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1478
ID AAE24190 standard; protein; 527 AA.
DE Human tissue plasminogen activator (tPA) protein.
PN MO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1479
ID AAG79362 standard; protein; 527 AA.
DE Human tissue plasminogen activator.
PN MO200243747-A2.
PD 06-JUN-2002.
PA (ISIS-) ISIS INNOVATION LTD.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1480
ID AAE25044 standard; protein; 527 AA.
DE Human tissue plasminogen activator (tPA) protein.
PN MO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1481
ID ADL92126 standard; protein; 527 AA.
DE Alteplase protein sequence.
PN MO2003099862-A1.
PD 04-DEC-2003.
PA (NANO-) APPLIED NANOSYSTEMS BV.
Query Match 7.1%; Score 280; DB 8; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1482
ID AED66381 standard; protein; 528 AA.
DE Recombinant human tissue type plasminogen activator (tPA) protein.
PN KR2005018231-A.
PD 23-FEB-2005.
PA (BIOB-) BIOBUD CO LTD.
Query Match 7.1%; Score 280; DB 9; Length 528;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1483
ID ABM82630 standard; protein; 534 AA.
DE Human diagnostic and therapeutic proprotein SEQ ID NO:2879.
PN MO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.1%; Score 280; DB 8; Length 534;
Best Local Similarity 22.7%; Pred. No. 3.8e-07;
RESULT 1484

ID ABM82821 standard; protein; 534 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3070.
PN MO2004023973-A2.
PD 25-MAR-2004.
PA (INCYT-) INCYTE CORP.
Query Match 7.1%; Score 280; DB 8; Length 534;
Best Local Similarity 22.7%; Pred. No. 3.8e-07;
RESULT 1485
ID AAR13020 standard; protein; 557 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (4).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 557;
Best Local Similarity 23.0%; Pred. No. 3.9e-07;
RESULT 1486
ID AAR13149 standard; protein; 557 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (4).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 557;
Best Local Similarity 23.0%; Pred. No. 3.9e-07;
RESULT 1487
ID AAP50219 standard; protein; 561 AA.
DE Tissue plasminogen activator encoded by cDNA clone.
PN EP143081-A.
PD 29-MAY-1985.
PA (CIBA) CIBA GEIGY AG.
Query Match 7.1%; Score 280; DB 1; Length 561;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1488
ID AAP60790 standard; protein; 562 AA.
DE Sequence of human pre-tissue plasminogen activator (pre-t-PA).
PN GB2137804-A.
PD 22-OCT-1986.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1489
ID AAP60810 standard; protein; 562 AA.
DE Sequence of modified human tissue plasminogen activator (t-PA).
PN FR2581652-A.
PD 14-NOV-1986.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1490
ID AAP60214 standard; protein; 562 AA.
DE Sequence of active human uterine tissue plasminogen activator (UTPA).
PN EP178105-A.
PD 16-APR-1986.
PA (INTE-) INTEG GENETICS INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1491
ID AAP81913 standard; protein; 562 AA.
DE Tissue plasminogen activator encoded by pEMpl-CPA.
PN WO8800242-A.
PD 14-JAN-1988.
PA (DAMO-) DAMON BIOTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1492
ID AAP80655 standard; protein; 562 AA.
DE Tissue plasminogen activator analogue.
PN EP293934-A.
PD 07-DEC-1988.
PA (ZYMO) ZYMOGENETICS INC.
PA (NOVO) NOVO IND AS.
PA (EISA) EISA CO LTD.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1493
ID AAP94406 standard; protein; 562 AA.
DE Sequence encoded by native tPA of plasmid pST112.
PN EP102456-A.
PD 08-FEB-1989.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1494
ID AAP93716 standard; protein; 562 AA.
DE Human melanoma t-PA encoded by plasmid pK612.
PN EP297066-A.
PD 28-DEC-1988.
PA (KABI) KABI GEN AB.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1495
ID AAP90916 standard; protein; 562 AA.
DE Human tissue plasminogen activator.
PN JP01174388-A.
PD 10-JUL-1989.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1496
ID AAR09288 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT11 (Ser 67, Leu 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1497
ID AAR06237 standard; protein; 562 AA.
DE Novel tissue plasminogen activator (tPA) encoded by plasmid pST112.
PN EP379890-A.
PD 01-AUG-1990.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1498
ID AAR04700 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA C87S, H420S
DE with altered residues 419 and 420.
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1499
ID AAR04701 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA K419S with
DE altered residue 419.
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;
RESULT 1500
ID AAR04699 standard; protein; 562 AA.
DE Native tissue plasminogen activator (t-PA).
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 4e-07;

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OM protein - protein search, using sw model

Run on: April 4, 2007, 22:20:34 ; Search time 187 Seconds
(without alignments)
1785.501 Million cell updates/sec

Perfect score: 3945
Sequence: 1 MELGWTQGLTFLQLLLIS.....LSTAFKVLFPKWIERNMK 720

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 46321458 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
27	3945	100.0	720	3	US-09-997-428-231
562	3945	100.0	720	4	US-10-174-587-170
626	3945	100.0	720	4	US-10-063-742-38
741	3945	100.0	720	5	US-10-972-317-38
743	3945	100.0	720	5	US-10-950-374-231
751	3945	100.0	720	6	US-11-102-240-38
752	3945	100.0	720	6	US-11-103-195-38
753	3939	99.8	720	4	US-10-004-551-4
754	3939	99.8	720	4	US-10-098-871-26
755	3939	99.8	720	6	US-11-045-029-4
756	3921.5	99.4	727	4	US-10-408-765A-1796
757	3500.5	88.7	649	4	US-10-274-639-17
758	3500.5	88.7	649	4	US-10-333-574-17
759	3089.5	78.3	567	4	US-10-004-551-2
760	3089.5	78.3	567	6	US-11-045-029-2
761	2946.5	74.7	570	4	US-10-067-422-9
762	2413	61.2	455	3	US-09-833-245-1401
763	2413	61.2	455	6	US-11-264-096-1401
764	1708.5	43.3	323	6	US-09-833-245-1402
765	1708.5	43.3	323	6	US-11-264-096-1402
766	949	24.1	181	5	US-10-756-149-4828
767	672	17.0	1019	4	US-10-183-992-4
768	672	17.0	1019	5	US-10-480-254-4
769	665	16.9	1019	4	US-10-183-992-8
770	665	16.9	1019	4	US-10-638-125-4
771	665	16.9	1019	5	US-10-480-254-8
772	665	16.9	1083	4	US-10-183-992-6
773	665	16.9	1083	4	US-10-638-125-2

774	665	16.9	1083	5	US-10-480-254-6	Sequence 6, Appl1
775	478	12.1	699	4	US-11-150-887-43	Sequence 43, Appl1
776	476	12.1	699	4	US-10-388-322-2	Sequence 2, Appl1
777	475	12.0	699	5	US-10-820-155-93	Sequence 93, Appl1
778	475	12.0	704	5	US-10-989-891-148	Sequence 148, Appl1
779	471	11.9	728	4	US-10-148-671-5	Sequence 5, Appl1
780	469.5	11.9	679	3	US-09-874-198-6	Sequence 6, Appl1
781	469.5	11.9	679	3	US-09-874-238-6	Sequence 6, Appl1
782	469.5	11.9	679	6	US-11-032-149-6	Sequence 6, Appl1
783	468	11.9	728	4	US-10-388-322-4	Sequence 4, Appl1
784	468	11.9	728	5	US-10-820-155-92	Sequence 92, Appl1
785	461	11.7	670	6	US-10-239-032-1	Sequence 1, Appl1
786	423	10.7	670	6	US-11-150-883-55	Sequence 55, Appl1
787	423	10.7	685	6	US-11-150-883-54	Sequence 54, Appl1
788	412	10.4	670	6	US-11-150-883-52	Sequence 52, Appl1
789	412	10.4	686	3	US-11-150-883-51	Sequence 51, Appl1
790	403.5	10.2	688	3	US-09-874-198-7	Sequence 7, Appl1
791	403.5	10.2	688	3	US-09-874-238-7	Sequence 7, Appl1
792	403.5	10.2	688	6	US-11-032-149-7	Sequence 7, Appl1
793	403.5	10.2	705	3	US-09-808-602-94	Sequence 94, Appl1
794	403.5	10.2	705	3	US-09-800-198-81	Sequence 81, Appl1
795	403.5	10.2	705	4	US-10-257-021-66	Sequence 66, Appl1
796	403.5	10.2	705	5	US-10-287-436A-452	Sequence 452, Appl1
797	403.5	10.2	705	5	US-10-287-436A-1152	Sequence 1152, Appl1
798	403.5	10.2	705	5	US-10-989-891-144	Sequence 144, Appl1
799	403.5	10.2	705	5	US-10-821-234-1532	Sequence 1532, Appl1
800	401.5	10.2	686	3	US-09-874-198-2	Sequence 2, Appl1
801	401.5	10.2	686	3	US-09-874-238-2	Sequence 2, Appl1
802	401.5	10.2	686	5	US-10-974-148-12	Sequence 12, Appl1
803	401.5	10.2	686	5	US-10-820-155-90	Sequence 90, Appl1
804	401.5	10.2	686	5	US-10-820-155-90	Sequence 90, Appl1
805	401.5	10.2	686	5	US-10-756-148-4705	Sequence 4705, Appl1
806	401.5	10.2	686	6	US-11-032-149-2	Sequence 2, Appl1
807	401.5	10.2	686	6	US-11-150-883-5	Sequence 5, Appl1
808	400.5	10.2	686	6	US-11-150-887-5	Sequence 5, Appl1
809	400.5	10.2	686	4	US-10-388-322-3	Sequence 3, Appl1
810	400.5	10.2	686	4	US-10-332-713-2	Sequence 2, Appl1
811	399.5	10.1	671	6	US-11-150-883-6	Sequence 6, Appl1
812	399.5	10.1	671	6	US-11-150-887-6	Sequence 6, Appl1
813	398.5	10.1	671	6	US-10-332-713-3	Sequence 3, Appl1
814	336	8.5	760	3	US-09-925-301-1024	Sequence 1024, Appl1
815	334	8.5	673	3	US-09-874-198-8	Sequence 8, Appl1
816	334	8.5	673	3	US-09-874-238-8	Sequence 8, Appl1
817	334	8.5	673	6	US-11-032-149-8	Sequence 8, Appl1
818	334	8.5	688	5	US-10-820-155-81	Sequence 81, Appl1
819	334	8.5	688	5	US-10-287-436A-99	Sequence 99, Appl1
820	334	8.5	688	5	US-10-287-436A-1256	Sequence 1256, Appl1
821	334	8.5	688	5	US-10-631-467-644	Sequence 644, Appl1
822	334	8.5	688	5	US-10-989-891-143	Sequence 143, Appl1
823	334	8.5	688	5	US-10-821-234-1533	Sequence 1533, Appl1
824	334	8.5	688	6	US-11-169-041-149	Sequence 149, Appl1
825	332	8.4	855	4	US-10-072-012-354	Sequence 354, Appl1
826	332	8.4	855	4	US-10-072-012-420	Sequence 420, Appl1
827	332	8.4	855	4	US-10-037-417-132	Sequence 132, Appl1
828	332	8.4	855	6	US-11-019-711-132	Sequence 132, Appl1
829	331.5	8.4	1019	3	US-09-776-197-64	Sequence 64, Appl1
830	331.5	8.4	1019	4	US-10-157-031-267	Sequence 267, Appl1
831	331.5	8.4	1019	4	US-10-156-214A-31	Sequence 31, Appl1
832	331.5	8.4	1019	4	US-10-729-807-37	Sequence 37, Appl1
833	330.5	8.4	1019	4	US-10-408-765A-2243	Sequence 2243, Appl1
834	329.5	8.4	3389	4	US-10-016-248-47	Sequence 47, Appl1
835	329.5	8.4	3389	4	US-10-408-765A-2286	Sequence 2286, Appl1
836	329.5	8.4	3308	4	US-10-016-248-47	Sequence 46, Appl1
837	329.5	8.4	3367	5	US-10-453-377-1112	Sequence 1112, Appl1
838	329.5	8.3	3364	4	US-10-016-248-45	Sequence 45, Appl1
839	328.5	8.3	1274	4	US-10-467-024-11	Sequence 11, Appl1
840	328.5	8.3	1274	6	US-11-046-866-11	Sequence 11, Appl1
841	328.5	8.3	1783	4	US-10-276-934-12	Sequence 12, Appl1
842	328.5	8.3	1800	4	US-10-276-934-10	Sequence 10, Appl1
843	328.5	8.3	1826	4	US-10-276-934-9	Sequence 9, Appl1
844	328.5	8.3	2008	4	US-10-276-934-11	Sequence 11, Appl1
845	328.5	8.3	2306	4	US-10-276-934-14	Sequence 14, Appl1
846	328.5	8.3	2352	4	US-10-276-934-13	Sequence 13, Appl1

847	328	8.3	762	4	US-10-729-807-1	Sequence 1, Appl1	920	309.5	7.8	799	4	US-10-072-012-410	Sequence 410, App
848	328	8.3	851	4	US-10-276-774-1798	Sequence 1798, Ap	921	309.5	7.8	799	4	US-10-072-012-416	Sequence 416, App
849	328	8.3	851	4	US-10-296-115-1143	Sequence 1185, Ap	922	309	7.8	799	4	US-10-182-263-3	Sequence 3, Appl1
850	328	8.3	855	4	US-10-295-027-1185	Sequence 353, App	923	309	7.8	799	4	US-10-182-263-5	Sequence 5, Appl1
851	328	8.3	855	4	US-10-072-012-353	Sequence 412, App	924	308	7.8	799	4	US-10-182-263-4	Sequence 4, Appl1
852	328	8.3	855	4	US-10-072-012-412	Sequence 419, App	925	301.5	7.6	799	4	US-09-825-751A-72	Sequence 72, Appl1
853	328	8.3	855	4	US-10-072-012-419	Sequence 612, App	926	301.5	7.6	799	4	US-10-851-438-72	Sequence 72, Appl1
854	327.5	8.3	449	3	US-09-925-302-612	Sequence 612, App	927	299.5	7.6	799	4	US-10-406-031-2	Sequence 2, Appl1
855	327.5	8.3	449	3	US-09-925-302-612	Sequence 612, App	928	298	7.6	799	4	US-10-104-047-394	Sequence 3904, Ap
856	327	8.3	688	4	US-10-453-827-884	Sequence 884, App	929	298	7.6	799	4	US-11-072-512-394	Sequence 3904, Ap
857	327	8.3	757	4	US-10-072-012-44	Sequence 44, Appl	930	296	7.5	799	4	US-10-051-874-101	Sequence 101, App
858	327	8.3	855	3	US-09-776-191-2	Sequence 2, Appl1	931	296	7.5	799	4	US-09-981-151A-87	Sequence 87, Appl1
859	327	8.3	855	3	US-10-099-700A-2	Sequence 2, Appl1	932	296	7.5	799	4	US-09-981-151A-96	Sequence 96, Appl1
860	327	8.3	855	4	US-10-190-0308-2	Sequence 2, Appl1	933	296	7.5	799	4	US-10-032-198-66	Sequence 66, Appl1
861	327	8.3	855	4	US-10-302-840A-2	Sequence 2, Appl1	934	296	7.5	799	4	US-10-074-978A-222	Sequence 222, App
862	327	8.3	855	4	US-10-267-219-2	Sequence 2, Appl1	935	296	7.5	799	4	US-10-074-978A-222	Sequence 222, App
863	327	8.3	855	4	US-10-112-221A-2	Sequence 2, Appl1	936	296	7.5	799	4	US-10-055-569A-96	Sequence 96, Appl1
864	327	8.3	855	4	US-10-104-271-2	Sequence 2, Appl1	937	296	7.5	799	4	US-10-042-865-155	Sequence 155, App
865	327	8.3	855	4	US-10-147-211A-2	Sequence 2, Appl1	938	296	7.5	799	4	US-10-072-012-804	Sequence 804, App
866	327	8.3	855	4	US-10-156-214A-2	Sequence 2, Appl1	939	296	7.5	799	4	US-10-072-012-812	Sequence 812, App
867	327	8.3	855	4	US-10-072-012-352	Sequence 352, App	940	296	7.5	799	4	US-10-037-417-135	Sequence 135, App
868	327	8.3	855	4	US-10-072-012-411	Sequence 411, App	941	296	7.5	799	4	US-11-019-711-135	Sequence 135, App
869	327	8.3	855	4	US-10-072-012-418	Sequence 418, App	942	296	7.5	799	4	US-10-450-763-51801	Sequence 51801, A
870	327	8.3	855	4	US-10-600-187-2	Sequence 2, Appl1	943	293	7.4	799	4	US-10-114-153-50	Sequence 50, Appl1
871	327	8.3	855	4	US-10-612-4668-2	Sequence 2, Appl1	944	291.5	7.4	799	4	US-10-741-600-909	Sequence 909, App
872	327	8.3	855	5	US-11-104-110-1	Sequence 1, Appl1	945	291.5	7.4	799	4	US-10-995-561-559	Sequence 559, App
873	327	8.3	855	6	US-11-104-111-22	Sequence 22, Appl	946	291	7.4	799	4	US-10-406-031-31	Sequence 31, Appl1
874	324	8.2	3095	6	US-11-235-732-4	Sequence 4, Appl1	947	289.5	7.3	799	4	US-09-776-191-10	Sequence 10, Appl1
875	321	8.1	3110	5	US-10-453-372-42	Sequence 42, Appl	948	289.5	7.3	799	4	US-10-156-214A-10	Sequence 10, Appl1
876	321	8.1	3546	5	US-10-453-372-32	Sequence 32, Appl	949	289.5	7.3	799	4	US-09-776-191-8	Sequence 8, Appl1
877	321	8.1	3546	5	US-10-453-372-32	Sequence 32, Appl	950	288.5	7.3	799	4	US-10-156-214A-8	Sequence 8, Appl1
878	319.5	8.1	455	4	US-10-406-031-17	Sequence 17, Appl	951	288.5	7.3	799	4	US-09-888-615-113	Sequence 113, App
879	318	8.1	2612	5	US-10-453-372-38	Sequence 38, Appl	952	288.5	7.3	799	4	US-10-167-749-169	Sequence 169, App
880	318	8.1	2669	5	US-10-453-372-36	Sequence 36, Appl	953	288.5	7.3	799	4	US-10-170-481A-169	Sequence 169, App
881	318	8.1	2669	5	US-10-453-372-36	Sequence 36, Appl	954	288.5	7.3	799	4	US-10-210-028-169	Sequence 169, App
882	318	8.1	3104	4	US-10-016-248-2	Sequence 2, Appl1	955	288.5	7.3	799	4	US-10-162-521A-169	Sequence 169, App
883	318	8.1	3104	5	US-10-453-372-34	Sequence 34, Appl	956	288.5	7.3	799	4	US-10-918-851-169	Sequence 169, App
884	318	8.1	3104	5	US-10-453-372-62	Sequence 62, Appl	957	288.5	7.3	799	4	US-10-805-667-169	Sequence 169, App
885	318	8.1	3104	5	US-10-453-372-64	Sequence 64, Appl	958	288.5	7.3	799	4	US-10-897-359-169	Sequence 169, App
886	317.5	8.0	3069	6	US-11-235-732-2	Sequence 2, Appl1	959	288.5	7.3	799	4	US-10-893-802-169	Sequence 169, App
887	317.5	8.0	3100	6	US-11-235-732-7	Sequence 7, Appl1	960	288.5	7.3	799	4	US-10-897-362-169	Sequence 169, App
888	317.5	8.0	454	4	US-10-406-031-11	Sequence 11, Appl	961	288.5	7.3	799	4	US-11-129-762-169	Sequence 169, App
889	314	8.0	855	3	US-09-900-751-2	Sequence 2, Appl	962	288.5	7.3	799	4	US-11-037-743-113	Sequence 113, App
890	314	8.0	855	4	US-10-072-012-355	Sequence 355, App	963	288.5	7.3	799	4	US-10-333-743-3	Sequence 3, Appl1
891	314	8.0	855	4	US-10-072-012-413	Sequence 413, App	964	288.5	7.3	799	4	US-10-600-187-10	Sequence 10, Appl
892	313	7.9	855	4	US-10-072-012-356	Sequence 356, App	965	288.5	7.3	799	4	US-10-297-987B-11	Sequence 11, Appl
893	313	7.9	855	4	US-10-072-012-414	Sequence 414, App	966	287	7.3	799	4	US-10-406-031-5	Sequence 5, Appl1
894	313	7.9	855	4	US-10-072-012-417	Sequence 417, App	967	283	7.2	799	4	US-10-865-978-25	Sequence 25, Appl1
895	312	7.9	855	4	US-10-168-407-5	Sequence 5, Appl	968	281	7.1	799	4	US-10-348-504-44	Sequence 44, Appl1
896	312	7.9	467	4	US-10-406-031-8	Sequence 8, Appl1	969	281	7.1	799	4	US-10-407-123-27	Sequence 27, Appl1
897	312	7.9	1031	4	US-10-451-168-80	Sequence 80, Appl	970	280	7.1	799	4	US-09-987-457-18	Sequence 18, Appl1
898	312	7.9	1031	5	US-10-980-387-80	Sequence 80, Appl	971	280	7.1	799	4	US-09-987-457-18	Sequence 18, Appl1
899	311	7.9	419	4	US-10-168-407-3	Sequence 3, Appl1	972	280	7.1	799	4	US-10-360-101-203	Sequence 203, App
900	311	7.9	419	4	US-10-168-407-6	Sequence 6, Appl1	973	280	7.1	799	4	US-10-705-633-1	Sequence 1, Appl1
901	310.5	7.9	409	5	US-10-506-301-2	Sequence 2, Appl1	974	280	7.1	799	4	US-10-742-887-51	Sequence 51, Appl
902	310.5	7.9	410	5	US-10-506-301-1	Sequence 1, Appl1	975	280	7.1	799	4	US-10-113-385-19	Sequence 19, Appl
903	310.5	7.9	415	4	US-10-670-628-2	Sequence 2, Appl1	976	280	7.1	799	4	US-09-869-271-7	Sequence 7, Appl1
904	310.5	7.9	419	3	US-09-997-623-4	Sequence 4, Appl1	977	280	7.1	799	4	US-09-974-298-145	Sequence 145, App
905	310.5	7.9	419	3	US-09-978-917A-4	Sequence 4, Appl1	978	280	7.1	799	4	US-10-443-701-4	Sequence 4, Appl1
906	310.5	7.9	419	4	US-10-182-263-1	Sequence 1, Appl1	979	280	7.1	799	4	US-10-193-656-8	Sequence 8, Appl1
907	310.5	7.9	419	4	US-10-168-407-1	Sequence 1, Appl1	980	280	7.1	799	4	US-10-411-037-26	Sequence 26, Appl
908	310.5	7.9	419	5	US-10-506-301-3	Sequence 3, Appl1	981	280	7.1	799	4	US-10-411-037-26	Sequence 26, Appl
909	310.5	7.9	419	5	US-10-492-191-1	Sequence 1, Appl1	982	280	7.1	799	4	US-10-411-037-26	Sequence 26, Appl
910	310.5	7.9	419	6	US-11-004-111-4	Sequence 4, Appl1	983	280	7.1	799	4	US-10-411-037-26	Sequence 26, Appl
911	310.5	7.9	453	4	US-10-406-031-14	Sequence 14, Appl	984	280	7.1	799	4	US-10-110-962-26	Sequence 26, Appl
912	310.5	7.9	461	3	US-09-997-623-2	Sequence 2, Appl1	985	280	7.1	799	4	US-10-411-037-26	Sequence 26, Appl
913	310.5	7.9	461	3	US-09-978-917A-2	Sequence 2, Appl1	986	280	7.1	799	4	US-10-411-037-26	Sequence 26, Appl
914	310.5	7.9	461	4	US-10-182-263-2	Sequence 2, Appl1	987	280	7.1	799	4	US-10-287-994-26	Sequence 26, Appl
915	310.5	7.9	461	5	US-10-168-407-2	Sequence 2, Appl1	988	280	7.1	799	4	US-10-410-913-26	Sequence 26, Appl
916	310.5	7.9	461	6	US-11-004-111-2	Sequence 2, Appl1	989	280	7.1	799	4	US-10-712-124-108	Sequence 108, App
917	310.5	7.9	461	6	US-11-004-111-2	Sequence 2, Appl1	990	280	7.1	799	4	US-10-741-600-911	Sequence 911, App
918	310	7.9	419	4	US-10-168-263-6	Sequence 6, Appl1	991	280	7.1	799	4	US-10-410-980-26	Sequence 26, Appl
919	310	7.9	419	4	US-10-168-407-4	Sequence 4, Appl1	992	280	7.1	799	4	US-10-410-980-26	Sequence 26, Appl

1080	280	7.1	562	5	US-10-410-897-26	Sequence 26, App1	1153	275.5	7.0	444	4	US-10-410-997-8	Sequence 8, App1
1081	280	7.1	562	5	US-10-492-261-26	Sequence 26, App1	1154	275.5	7.0	444	4	US-10-411-012-8	Sequence 8, App1
1082	280	7.1	562	5	US-10-995-561-561	Sequence 561, App	1155	275.5	7.0	444	4	US-10-287-994-8	Sequence 8, App1
1083	280	7.1	562	6	US-11-169-041-153	Sequence 153, App	1156	275.5	7.0	444	4	US-10-410-913-8	Sequence 8, App1
1084	280	7.1	562	6	US-11-183-205-26	Sequence 26, App1	1157	275.5	7.0	444	4	US-10-738-777-3	Sequence 8, App1
1085	279.5	7.1	782	4	US-10-097-340-312	Sequence 312, App	1158	275.5	7.0	444	5	US-10-410-980-8	Sequence 8, App1
1086	279.5	7.1	782	6	US-11-050-926-312	Sequence 312, App	1159	275.5	7.0	444	5	US-10-410-987-8	Sequence 8, App1
1087	279	7.1	527	4	US-10-705-633-2	Sequence 2, App1	1160	275.5	7.0	444	5	US-10-492-261-8	Sequence 8, App1
1088	279	7.1	932	6	US-10-363-937-6	Sequence 6, App1	1161	275.5	7.0	444	6	US-11-183-205-8	Sequence 8, App1
1089	279	7.1	932	6	US-11-167-040-6	Sequence 6, App1	1162	275.5	7.0	459	4	US-10-741-601-503	Sequence 503, App
1090	279	7.1	970	3	US-09-888-615-101	Sequence 101, App	1163	275.5	7.0	459	4	US-10-741-601-504	Sequence 504, App
1091	279	7.1	970	6	US-11-037-243-101	Sequence 101, App	1164	275.5	7.0	641	4	US-10-617-619-8	Sequence 8, App1
1092	278.5	7.1	264	3	US-09-978-418-34	Sequence 34, App1	1165	275.5	7.0	641	6	US-11-227-340-8	Sequence 8, App1
1093	278.5	7.1	264	5	US-10-485-231-34	Sequence 34, App1	1166	275.5	7.0	671	5	US-10-841-250-6	Sequence 6, App1
1094	278.5	7.1	466	4	US-10-017-122-2	Sequence 2, App1	1167	275.5	7.0	671	5	US-11-029-003-6	Sequence 6, App1
1095	278.5	7.1	466	4	US-10-375-741-14	Sequence 14, App1	1168	275.5	7.0	679	4	US-10-617-619-11	Sequence 11, App1
1096	278.5	7.1	481	4	US-10-741-601-501	Sequence 501, App	1169	275.5	7.0	679	6	US-11-227-340-11	Sequence 11, App1
1097	278.5	7.1	481	4	US-10-741-601-502	Sequence 502, App	1170	275	7.0	1113	5	US-10-926-083-4	Sequence 4, App1
1098	278.5	7.1	701	6	US-10-617-619-6	Sequence 6, App1	1171	273	6.9	560	3	US-09-912-559-3	Sequence 3, App1
1099	278.5	7.1	701	6	US-11-097-143-42048	Sequence 42048, A	1172	273	6.9	560	3	US-09-912-559-4	Sequence 4, App1
1100	278	7.0	488	4	US-10-464-368-78	Sequence 78, App1	1173	273	6.9	560	4	US-10-172-712-32	Sequence 32, App1
1101	278	7.0	488	4	US-10-464-368-78	Sequence 78, App1	1174	273	6.9	560	4	US-10-391-215-5	Sequence 5, App1
1102	278	7.0	488	5	US-10-723-860-261	Sequence 261, App	1175	273	6.9	560	4	US-10-391-215-6	Sequence 6, App1
1103	278	7.0	488	5	US-10-492-191-23	Sequence 23, App1	1176	273	6.9	560	4	US-10-391-215-7	Sequence 7, App1
1104	278	7.0	1113	4	US-10-464-368-78	Sequence 78, App1	1177	273	6.9	560	4	US-10-391-215-8	Sequence 8, App1
1105	278	7.0	1113	6	US-11-067-811-4	Sequence 4, App1	1178	273	6.9	560	5	US-10-719-993-854	Sequence 854, App
1106	277.5	7.0	476	5	US-10-494-004-1	Sequence 1, App1	1179	273	6.9	560	5	US-10-930-754-3	Sequence 3, App1
1107	276.5	7.0	426	3	US-09-951-121A-1	Sequence 1, App1	1180	273	6.9	560	5	US-10-930-754-4	Sequence 4, App1
1108	276.5	7.0	426	3	US-09-848-107-1	Sequence 1, App1	1181	273	6.9	560	5	US-10-930-754-5	Sequence 5, App1
1109	276.5	7.0	426	3	US-10-295-682-1	Sequence 1, App1	1182	272.5	6.9	296	4	US-10-756-149-5450	Sequence 5450, App
1110	276.5	7.0	655	4	US-10-172-712-28	Sequence 28, App1	1183	272	6.9	488	4	US-10-148-671-17	Sequence 17, App1
1111	276	7.0	249	3	US-09-961-721-5	Sequence 5, App1	1184	271.5	6.9	244	4	US-10-712-332-1	Sequence 1, App1
1112	276	7.0	249	3	US-10-170-789-46	Sequence 46, App1	1185	271.5	6.9	244	4	US-10-097-340-169	Sequence 169, App
1113	276	7.0	249	3	US-11-151-601-28	Sequence 28, App1	1186	271.5	6.9	244	4	US-10-282-907-2	Sequence 2, App1
1114	276	7.0	251	3	US-09-961-721-4	Sequence 4, App1	1187	271.5	6.9	244	4	US-10-301-822-97	Sequence 97, App1
1115	276	7.0	251	4	US-10-170-789-45	Sequence 45, App1	1188	271.5	6.9	244	4	US-10-295-027-550	Sequence 530, App
1116	276	7.0	251	6	US-11-151-601-27	Sequence 27, App1	1189	271.5	6.9	244	4	US-10-173-999-131	Sequence 131, App
1117	276	7.0	259	4	US-10-107-782-214	Sequence 214, App	1190	271.5	6.9	244	4	US-10-344-394-25	Sequence 25, App1
1118	276	7.0	359	4	US-10-038-854-100	Sequence 100, App	1191	271.5	6.9	244	4	US-10-757-262-28	Sequence 28, App1
1119	276	7.0	396	4	US-10-700-778-1	Sequence 1, App1	1192	271.5	6.9	244	5	US-10-868-490A-11	Sequence 9, App1
1120	276	7.0	527	4	US-10-705-633-3	Sequence 3, App1	1193	271.5	6.9	244	5	US-10-868-490A-13	Sequence 13, App1
1121	275.5	7.0	405	4	US-10-360-101-225	Sequence 225, App	1194	271.5	6.9	244	5	US-10-868-490A-15	Sequence 15, App1
1122	275.5	7.0	406	3	US-09-782-587B-1	Sequence 1, App1	1195	271.5	6.9	244	5	US-10-961-139-14	Sequence 14, App1
1123	275.5	7.0	406	3	US-09-782-587B-3	Sequence 3, App1	1196	271.5	6.9	244	5	US-10-756-149-4863	Sequence 4963, App
1124	275.5	7.0	406	4	US-10-109-498-1	Sequence 1, App1	1197	271.5	6.9	244	6	US-11-050-926-169	Sequence 169, App
1125	275.5	7.0	406	4	US-10-255-032-1	Sequence 1, App1	1198	271.5	6.9	244	6	US-11-186-284-97	Sequence 97, App1
1126	275.5	7.0	406	4	US-10-281-727-1	Sequence 1, App1	1199	271.5	6.9	244	6	US-11-050-857-670	Sequence 670, App
1127	275.5	7.0	406	4	US-10-386-898-7	Sequence 7, App1	1200	271.5	6.9	253	6	US-11-050-857-671	Sequence 671, App
1128	275.5	7.0	406	4	US-10-383-898-1	Sequence 1, App1	1201	271.5	6.9	1006	4	US-10-210-130-62	Sequence 62, App1
1129	275.5	7.0	406	4	US-10-617-500-1	Sequence 1, App1	1202	271	6.9	650	4	US-10-401-077-1	Sequence 1, App1
1130	275.5	7.0	406	4	US-10-263-205B-2	Sequence 2, App1	1203	269	6.8	462	4	US-10-416-952-2	Sequence 2, App1
1131	275.5	7.0	406	4	US-10-617-619-1	Sequence 1, App1	1204	269	6.8	643	3	US-09-808-602-103	Sequence 103, App
1132	275.5	7.0	406	4	US-10-701-294-1	Sequence 1, App1	1205	269	6.8	643	3	US-09-800-139-86	Sequence 86, App1
1133	275.5	7.0	406	4	US-10-669-537-1	Sequence 1, App1	1206	269	6.8	643	4	US-10-099-332-113	Sequence 113, App
1134	275.5	7.0	406	4	US-10-738-777-2	Sequence 2, App1	1207	269	6.8	643	4	US-10-044-564-113	Sequence 113, App
1135	275.5	7.0	406	5	US-10-900-490-1	Sequence 1, App1	1208	269	6.8	643	6	US-11-054-281-113	Sequence 113, App
1136	275.5	7.0	406	5	US-10-725-843-3	Sequence 3, App1	1209	267	6.8	462	4	US-10-411-037-10	Sequence 10, App1
1137	275.5	7.0	406	5	US-10-609-701A-1	Sequence 1, App1	1210	267	6.8	462	4	US-10-411-026-10	Sequence 10, App1
1138	275.5	7.0	406	5	US-10-950-747-1	Sequence 1, App1	1211	267	6.8	462	4	US-10-410-962-10	Sequence 10, App1
1139	275.5	7.0	406	5	US-10-822-943-1	Sequence 3, App1	1212	267	6.8	462	4	US-10-411-049-10	Sequence 10, App1
1140	275.5	7.0	406	5	US-10-822-943-1	Sequence 3, App1	1213	267	6.8	462	4	US-10-410-930-10	Sequence 10, App1
1141	275.5	7.0	406	6	US-11-021-239-1	Sequence 1, App1	1214	267	6.8	462	4	US-10-410-997-10	Sequence 10, App1
1142	275.5	7.0	406	6	US-11-111-072-1	Sequence 1, App1	1215	267	6.8	462	4	US-10-411-012-10	Sequence 10, App1
1143	275.5	7.0	406	6	US-11-111-072-1	Sequence 1, App1	1216	267	6.8	462	4	US-10-287-994-10	Sequence 10, App1
1144	275.5	7.0	406	6	US-11-186-669-1	Sequence 1, App1	1217	267	6.8	462	4	US-10-410-913-10	Sequence 10, App1
1145	275.5	7.0	406	6	US-11-227-340-1	Sequence 1, App1	1218	267	6.8	462	5	US-10-410-980-10	Sequence 10, App1
1146	275.5	7.0	444	4	US-10-411-037-8	Sequence 8, App1	1219	267	6.8	462	5	US-10-410-897-10	Sequence 10, App1
1147	275.5	7.0	444	4	US-10-382-248-34	Sequence 34, App1	1220	267	6.8	462	5	US-10-492-261-10	Sequence 10, App1
1148	275.5	7.0	444	4	US-10-411-026-8	Sequence 8, App1	1221	267	6.8	462	6	US-11-183-205-10	Sequence 10, App1
1149	275.5	7.0	444	4	US-10-410-962-8	Sequence 8, App1	1222	265.5	6.7	250	6	US-11-097-143-24561	Sequence 24561, A
1150	275.5	7.0	444	4	US-10-411-049-8	Sequence 8, App1	1223	265	6.7	419	4	US-10-382-248-36	Sequence 36, App1
1151	275.5	7.0	444	4	US-10-263-205B-3	Sequence 3, App1	1224	264.5	6.7	900	5	US-10-865-978-15	Sequence 15, App1
1152	275.5	7.0	444	4	US-10-410-930-8	Sequence 8, App1	1225	264	6.7	431	4	US-10-247-671-149	Sequence 149, App

1226	263.5	6.7	411	4	US-10-744-927-1	Sequence 1, Appl1	1299	258.5	6.6	411	4	US-10-407-821-2	Sequence 2, Appl1
1227	263.5	6.7	494	6	US-11-094-519A-35	Sequence 35, Appl1	1300	258.5	6.5	411	5	US-10-828-531B-16	Sequence 16, Appl1
1228	263	6.7	431	4	US-10-076-421-2	Sequence 2, Appl1	1301	258.5	6.6	411	6	US-11-019-448-3	Sequence 3, Appl1
1229	263	6.7	431	4	US-10-171-311-184	Sequence 184, App	1302	258.5	6.6	412	5	US-10-825-911-2	Sequence 2, Appl1
1230	263	6.7	431	4	US-10-301-822-161	Sequence 161, App	1303	258.5	6.6	787	6	US-11-097-143-40698	Sequence 40698, A
1231	263	6.7	431	4	US-10-131-985-91	Sequence 21, Appl1	1304	257.5	6.5	591	5	US-10-865-978-17	Sequence 17, Appl1
1232	263	6.7	431	4	US-10-295-027-114	Sequence 414, App	1305	257	6.5	215	4	US-10-051-874-102	Sequence 102, App
1233	263	6.7	431	4	US-10-235-027-1275	Sequence 1275, App	1306	257	6.5	217	3	US-09-981-151A-88	Sequence 88, Appl1
1234	263	6.7	431	4	US-10-411-037-34	Sequence 34, Appl1	1307	257	6.5	217	3	US-09-981-151A-97	Sequence 97, Appl1
1235	263	6.7	431	4	US-10-411-026-34	Sequence 34, Appl1	1308	257	6.5	217	4	US-10-032-189-67	Sequence 67, Appl1
1236	263	6.7	431	4	US-10-410-962-34	Sequence 34, Appl1	1309	257	6.5	217	4	US-10-074-978A-223	Sequence 223, App
1237	263	6.7	431	4	US-10-411-049-34	Sequence 34, Appl1	1310	257	6.5	217	4	US-10-055-569A-97	Sequence 97, Appl1
1238	263	6.7	431	4	US-10-410-930-34	Sequence 34, Appl1	1311	257	6.5	217	4	US-10-042-865-156	Sequence 156, App
1239	263	6.7	431	4	US-10-410-997-34	Sequence 34, Appl1	1312	257	6.5	217	4	US-10-072-012-805	Sequence 805, App
1240	263	6.7	431	4	US-10-411-012-34	Sequence 34, Appl1	1313	257	6.5	217	4	US-10-072-012-813	Sequence 813, App
1241	263	6.7	431	4	US-10-287-994-34	Sequence 34, Appl1	1314	257	6.5	217	4	US-10-037-417-136	Sequence 136, App
1242	263	6.7	431	4	US-10-410-913-34	Sequence 34, Appl1	1315	257	6.5	217	6	US-11-019-711-136	Sequence 136, App
1243	263	6.7	431	5	US-10-741-600-1265	Sequence 1265, Ap	1316	257	6.5	529	4	US-10-398-037-2	Sequence 2, Appl1
1244	263	6.7	431	5	US-10-741-600-1266	Sequence 1266, Ap	1317	257	6.5	1039	5	US-10-865-978B-30	Sequence 30, Appl1
1245	263	6.7	431	5	US-10-901-417-31	Sequence 21, Appl1	1318	256	6.5	207	4	US-10-004-378A-147	Sequence 147, App
1246	263	6.7	431	5	US-10-410-980-34	Sequence 34, Appl1	1319	255.5	6.5	244	3	US-09-796-294-11	Sequence 11, Appl1
1247	263	6.7	431	5	US-10-645-756-38	Sequence 38, Appl1	1320	255.5	6.5	244	4	US-10-461-787-11	Sequence 11, Appl1
1248	263	6.7	431	5	US-10-410-897-34	Sequence 34, Appl1	1321	255.5	6.5	244	6	US-11-251-455-13	Sequence 13, Appl1
1249	263	6.7	431	5	US-10-492-261-34	Sequence 34, Appl1	1322	255.5	6.5	441	5	US-10-741-600-829	Sequence 829, App
1250	263	6.7	431	5	US-10-995-561-807	Sequence 807, App	1323	255.5	6.5	487	5	US-10-455-772-52	Sequence 52, Appl1
1251	263	6.7	431	5	US-10-995-561-808	Sequence 808, App	1324	254.5	6.5	437	4	US-10-455-772-3	GENERAL INFORMA
1252	263	6.7	431	6	US-11-186-284-161	Sequence 161, App	1325	254.5	6.5	466	5	US-10-455-772-24	Sequence 24, Appl1
1253	263	6.7	431	6	US-11-183-205-34	Sequence 34, Appl1	1326	254.5	6.5	487	5	US-10-455-772-48	Sequence 48, Appl1
1254	263	6.7	437	4	US-10-087-182-94	Sequence 594, App	1327	254	6.4	314	6	US-11-097-443-6243	Sequence 6243, Ap
1255	262.5	6.7	415	4	US-10-466-998A-2	Sequence 2, Appl1	1328	254	6.4	421	3	US-09-264-468B-11	Sequence 11, Appl1
1256	262.5	6.7	415	6	US-11-166-028-1	Sequence 1, Appl1	1329	253.5	6.4	466	5	US-10-455-772-22	Sequence 22, Appl1
1257	262.5	6.7	433	5	US-10-488-671-1	Sequence 1, Appl1	1330	253.5	6.4	444	3	US-09-808-602-95	Sequence 95, Appl1
1258	262.5	6.7	456	4	US-10-038-854-85	Sequence 95, Appl1	1331	253.5	6.4	487	3	US-09-808-602-93	Sequence 93, Appl1
1259	262.5	6.7	456	4	US-10-038-854-86	Sequence 96, Appl1	1332	253.5	6.4	487	3	US-09-800-198-80	Sequence 80, Appl1
1260	262.5	6.7	461	3	US-08-884-901-3	Sequence 3, Appl1	1333	253.5	6.4	487	5	US-10-455-772-16	Sequence 16, Appl1
1261	262.5	6.7	461	4	US-10-132-829-5	Sequence 5, Appl1	1334	253.5	6.4	487	5	US-10-455-772-46	Sequence 46, Appl1
1262	262.5	6.7	461	4	US-10-234-406-6	Sequence 6, Appl1	1335	253.5	6.4	487	5	US-10-455-772-50	Sequence 50, Appl1
1263	262.5	6.7	461	4	US-10-234-406-8	Sequence 8, Appl1	1336	253.5	6.4	1043	4	US-10-016-248-48	Sequence 48, Appl1
1264	262.5	6.7	461	4	US-10-133-907-5	Sequence 9, Appl1	1337	253.5	6.4	1048	4	US-10-016-248-48	Sequence 48, Appl1
1265	262.5	6.7	461	4	US-10-038-854-92	Sequence 92, Appl1	1338	253	6.4	273	4	US-10-148-671-25	Sequence 25, Appl1
1266	262.5	6.7	461	4	US-10-038-854-93	Sequence 93, Appl1	1339	253	6.4	423	5	US-10-455-772-26	Sequence 26, Appl1
1267	262.5	6.7	461	4	US-10-038-854-94	Sequence 94, Appl1	1340	252.5	6.4	487	3	US-09-808-602-21	Sequence 21, Appl1
1268	262.5	6.7	461	5	US-10-239-498A-5	Sequence 5, Appl1	1341	252.5	6.4	487	5	US-10-455-772-42	Sequence 42, Appl1
1269	262.5	6.7	461	5	US-10-741-600-832	Sequence 832, App	1342	252.5	6.4	466	5	US-10-455-772-18	Sequence 18, Appl1
1270	262.5	6.7	461	5	US-10-455-772-752	Sequence 752, App	1343	252.5	6.4	466	5	US-10-455-772-30	Sequence 30, Appl1
1271	262.5	6.7	461	5	US-10-455-772-754	Sequence 754, App	1344	252.5	6.4	487	5	US-10-455-772-40	Sequence 40, Appl1
1272	262.5	6.7	461	6	US-11-172-459-1	Sequence 1, Appl1	1345	252	6.4	487	5	US-10-865-978-16	Sequence 16, Appl1
1273	262.5	6.7	696	5	US-10-841-250-8	Sequence 8, Appl1	1346	252	6.4	889	5	US-10-865-978-22	Sequence 22, Appl1
1274	262.5	6.7	696	5	US-10-841-819B-23	Sequence 23, Appl1	1347	251.5	6.4	466	5	US-10-455-772-32	Sequence 32, Appl1
1275	262.5	6.7	696	6	US-11-029-003-8	Sequence 8, Appl1	1348	251.5	6.4	487	3	US-09-808-602-17	Sequence 17, Appl1
1276	262.5	6.7	1042	3	US-09-776-191-62	Sequence 29, Appl1	1349	251.5	6.4	487	3	US-09-808-602-19	Sequence 19, Appl1
1277	262.5	6.7	1042	4	US-10-156-214A-29	Sequence 29, Appl1	1350	251.5	6.4	487	3	US-09-800-198-17	Sequence 17, Appl1
1278	262.5	6.7	1042	5	US-10-865-978-2	Sequence 2, Appl1	1351	251.5	6.4	487	3	US-09-800-198-19	Sequence 19, Appl1
1279	262.5	6.7	1042	5	US-10-926-083-2	Sequence 2, Appl1	1352	251	6.4	487	3	US-10-792-966-5	Sequence 5, Appl1
1280	262.5	6.7	1044	6	US-11-067-811-1	Sequence 1, Appl1	1353	250	6.3	1379	6	US-11-097-143-3372	Sequence 3372, Ap
1281	262.5	6.7	1044	5	US-10-865-978-9	Sequence 9, Appl1	1354	249.5	6.3	403	3	US-09-880-503-6	Sequence 6, Appl1
1282	262.5	6.7	1076	4	US-10-276-774-2345	Sequence 2345, Ap	1355	249.5	6.3	403	6	US-11-019-448-6	Sequence 6, Appl1
1283	262	6.6	280	4	US-10-148-671-26	Sequence 26, Appl1	1356	249.5	6.3	822	3	US-09-147-947-6	Sequence 6, Appl1
1284	261.5	6.6	415	3	US-09-118-748-2	Sequence 2, Appl1	1357	249.5	6.3	822	3	US-09-147-947-6	Sequence 6, Appl1
1285	261.5	6.6	443	4	US-10-741-600-830	Sequence 830, App	1358	249.5	6.3	875	5	US-10-757-662-34	Sequence 34, Appl1
1286	261	6.6	431	4	US-10-193-656-4	Sequence 4, App	1359	249.5	6.3	875	5	US-10-743-860-4046	Sequence 4046, Ap
1287	261	6.6	431	5	US-10-723-860-870	Sequence 870, App	1360	249.5	6.3	966	3	US-09-283-699-2	Sequence 2, Appl1
1288	261	6.6	431	5	US-10-756-149-4928	Sequence 4928, Ap	1361	249	6.3	966	3	US-09-285-185C-19	Sequence 19, Appl1
1289	261	6.6	431	5	US-10-504-287-2	Sequence 2, Appl1	1362	249	6.3	225	3	US-09-776-191-6	Sequence 6, Appl1
1290	260.5	6.6	437	4	US-10-712-332-2	GENERAL INFORMA	1363	249	6.3	225	4	US-10-156-614A-6	Sequence 6, Appl1
1291	260.5	6.6	1032	5	US-10-719-993-814	Sequence 814, App	1364	249	6.3	251	3	US-09-789-210-47	Sequence 47, Appl1
1292	260	6.6	431	4	US-10-288-174-562	Sequence 562, App	1365	249	6.3	263	3	US-09-888-615-96	Sequence 96, Appl1
1293	259.5	6.6	431	5	US-10-600-009-562	Sequence 562, App	1366	248.5	6.3	260	3	US-11-037-443-96	Sequence 96, Appl1
1294	259.5	6.6	227	5	US-10-865-978-34	Sequence 34, Appl1	1367	248.5	6.3	260	3	US-09-898-637A-45	Sequence 45, Appl1
1295	259	6.6	227	4	US-10-045-367A-4	Sequence 4, Appl1	1368	248.5	6.3	260	3	US-09-210-51	Sequence 51, Appl1
1296	259	6.6	227	4	US-10-170-789-34	Sequence 54, Appl1	1369	248	6.3	261	3	US-09-898-637A-62	Sequence 62, Appl1
1297	259	6.6	227	6	US-11-151-601-36	Sequence 36, Appl1	1370	248	6.3	230	3	US-09-789-210-61	Sequence 61, Appl1
1298	258.5	6.6	411	3	US-09-880-503-3	Sequence 3, Appl1	1371	248	6.3	230	6	US-11-104-110-3	Sequence 3, Appl1
												US-11-104-111-24	Sequence 24, Appl1

1372	248	6.3	231	4	US-10-600-187-6	Sequence 6, Appl	1445	244	6.2	638	6	US-11-054-281-114	Sequence 114, App
1373	248	6.3	263	5	US-10-733-969A-74	Sequence 74, Appl	1446	243.5	6.2	435	6	US-11-097-143-41688	Sequence 41688, A
1374	248	6.3	638	3	US-09-808-602-102	Sequence 102, App	1447	243	6.2	273	4	US-10-028-248A-63	Sequence 63, Appl
1375	248	6.3	638	3	US-09-800-198-85	Sequence 85, Appl	1448	243	6.2	273	4	US-10-107-782-63	Sequence 63, Appl
1376	248	6.3	638	4	US-10-099-322-111	Sequence 111, App	1449	243	6.2	282	4	US-10-051-874-97	Sequence 97, Appl
1377	248	6.3	638	4	US-10-044-564-111	Sequence 111, App	1450	242.5	6.1	232	4	US-10-156-214A-276	Sequence 276, App
1378	248	6.3	638	4	US-10-403-161-50	Sequence 50, Appl	1451	242.5	6.1	326	5	US-10-865-978-37	Sequence 37, Appl
1379	248	6.3	638	4	US-10-287-226-400	Sequence 400, App	1452	242.5	6.1	326	5	US-10-865-978-37	Sequence 37, Appl
1380	248	6.3	638	4	US-10-287-226-658	Sequence 658, App	1453	242.5	6.1	610	5	US-10-921-793-4	Sequence 4, Appl
1381	248	6.3	638	4	US-10-741-601-303	Sequence 303, App	1454	242.5	6.1	610	5	US-10-931-198-4	Sequence 4, Appl
1382	248	6.3	638	5	US-10-741-600-854	Sequence 854, App	1455	242.5	6.1	730	5	US-10-942-042-4	Sequence 461, App
1383	248	6.3	638	6	US-10-995-561-536	Sequence 536, App	1456	242.5	6.1	730	5	US-10-942-042-4	Sequence 461, App
1384	247.5	6.3	635	4	US-11-054-281-111	Sequence 111, App	1457	242.5	6.1	730	5	US-10-921-793-2	Sequence 2, Appl
1385	247.5	6.3	635	4	US-10-741-601-304	Sequence 304, App	1458	242.5	6.1	730	5	US-10-921-793-2	Sequence 2, Appl
1386	247.5	6.3	635	5	US-10-741-600-855	Sequence 855, App	1459	242.5	6.1	730	5	US-10-942-042-2	Sequence 2, Appl
1387	247	6.3	364	6	US-11-097-143-28392	Sequence 28392, A	1460	242.5	6.1	1019	4	US-10-016-248-99	Sequence 99, Appl
1388	247	6.3	455	5	US-10-865-978-18	Sequence 18, Appl	1461	242.5	6.1	3371	4	US-10-603-283-2	Sequence 2, Appl
1389	247	6.3	619	4	US-10-403-161-52	Sequence 52, Appl	1462	242	6.1	332	4	US-10-114-270-134	Sequence 134, App
1390	247	6.3	623	4	US-10-287-226-404	Sequence 404, App	1463	242	6.1	597	5	US-10-453-375-54	Sequence 54, Appl
1391	247	6.3	638	4	US-10-403-161-48	Sequence 48, Appl	1464	241.5	6.1	730	3	US-09-850-048A-2	Sequence 2, Appl
1392	247	6.3	638	4	US-10-099-322-30	Sequence 30, Appl	1465	241.5	6.1	416	3	US-09-815-876-2	Sequence 2, Appl
1393	247	6.3	638	4	US-10-044-564-30	Sequence 30, Appl	1466	241.5	6.1	416	5	US-10-239-032-8	Sequence 8, Appl
1394	247	6.3	638	4	US-10-403-161-46	Sequence 46, Appl	1467	241.5	6.1	823	4	US-10-016-248-98	Sequence 98, Appl
1395	247	6.3	638	4	US-10-287-226-402	Sequence 402, App	1468	241	6.1	346	3	US-09-977-577-8	Sequence 8, Appl
1396	247	6.3	638	6	US-11-054-281-30	Sequence 30, Appl	1469	241	6.1	346	5	US-10-885-784-8	Sequence 8, Appl
1397	247	6.3	739	6	US-11-057-047-2	Sequence 2, Appl	1470	241	6.1	986	3	US-10-850-048A-4	Sequence 4, Appl
1398	247	6.3	764	4	US-10-177-293-27	Sequence 27, Appl	1471	240.5	6.1	278	3	US-09-813-432-12	Sequence 12, Appl
1399	247	6.3	764	4	US-10-236-031B-44	Sequence 44, Appl	1472	240.5	6.1	278	3	US-09-813-432-43	Sequence 43, Appl
1400	247	6.3	764	5	US-10-733-969A-4	Sequence 4, Appl	1473	240.5	6.1	278	4	US-10-174-364-12	Sequence 12, Appl
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1407	247	6.3	986	3	US-09-918-715-242	Sequence 342, App	1480	240.5	6.1	970	5	US-10-016-248-42	Sequence 42, Appl
1408	247	6.3	986	4	US-10-366-345-33	Sequence 242, App	1481	240.5	6.1	970	5	US-10-455-772-92	Sequence 92, Appl
1409	247	6.3	986	5	US-10-474-794-242	Sequence 474, App	1482	240.5	6.1	3571	3	US-09-911-842-2	Sequence 2, Appl
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1413	246.5	6.2	254	5	US-10-887-104-11	Sequence 11, Appl	1486	240	6.1	1128	4	US-09-888-615-97	Sequence 8, Appl
1414	246.5	6.2	259	5	US-09-789-210-52	Sequence 52, App	1487	240	6.1	1128	6	US-10-399-645-8	Sequence 8, Appl
1415	246.5	6.2	259	5	US-10-872-198-5	Sequence 5, Appl	1488	239.5	6.1	406	3	US-11-037-243-97	Sequence 97, Appl
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SUMMARIES

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7	3936	99.8	720	7	US-11-354-653-32
8	3923	99.4	720	7	US-11-001-793-8647
9	3921.5	99.4	727	6	US-10-529-348-1034
10	3828	97.0	699	7	US-11-354-653-86
11	3617	91.7	720	7	US-11-354-653-118
12	2413	61.2	455	7	US-11-001-793-10886
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14	580	14.7	103	6	US-10-631-441-2419
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17	468	11.9	728	6	US-10-527-191-13
18	403.5	10.2	688	7	US-11-476-754-7
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36	328	8.3	855	6	US-10-533-519-428	Sequence 428, App
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41	328	8.3	855	7	US-11-362-260A-338	Sequence 338, App
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52	310.5	7.9	461	7	US-11-397-046-3	Sequence 3, Appli
53	310.5	7.9	461	7	US-11-397-046-4	Sequence 4, Appli
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55	297.5	7.5	543	7	US-11-090-997-2034	Sequence 2034, Ap
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57	291.5	7.4	516	6	US-11-090-997-2038	Sequence 2038, Ap
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114	275.5	7.0	444	6	US-10-410-945-8	Sequence 8, Appl1	187	236.5	6.0	396	7	US-11-090-997-2032	Sequence 2032, Ap
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117	275.5	7.0	444	7	US-11-404-266-8	Sequence 8, Appl1	190	236	6.0	783	6	US-10-777-288A-2296	Sequence 2296, Ap
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137	263	6.7	431	6	US-10-505-928-465	Sequence 465, App	210	226	5.7	423	6	US-10-530-991-42	Sequence 42, App
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139	263	6.7	431	6	US-10-669-920-459	Sequence 459, App	215	226	5.7	432	7	US-11-376-673-112	Sequence 112, App
140	263	6.7	431	6	US-10-533-519-1049	Sequence 1049, Ap	216	226	5.7	432	7	US-11-102-284-112	Sequence 112, App
141	263	6.7	431	6	US-10-530-972-34	Sequence 34, Appl	217	226	5.7	437	6	US-10-529-348-1258	Sequence 1258, App
142	263	6.7	431	6	US-10-552-896-34	Sequence 34, Appl	218	226	5.7	437	7	US-11-371-354-13613	Sequence 13613, App
143	263	6.7	431	6	US-10-410-945-34	Sequence 34, Appl	219	226	5.7	437	7	US-11-371-354-66069	Sequence 66069, A
144	263	6.7	431	7	US-11-183-318-34	Sequence 34, Appl	220	226	5.7	437	7	US-11-371-354-78251	Sequence 78251, A
145	263	6.7	431	7	US-11-371-354-13081	Sequence 13081, A	221	225	5.7	290	7	US-11-327-490-4	Sequence 4, Appl1
146	263	6.7	431	7	US-11-371-354-75459	Sequence 75459, A	222	225	5.7	615	6	US-10-529-348-574	Sequence 574, App
147	263	6.7	431	7	US-11-371-354-77523	Sequence 77523, A	223	224.5	5.7	235	7	US-11-254-185-5	Sequence 5, Appl1
148	263	6.7	431	7	US-11-404-266-34	Sequence 34, Appl	224	224.5	5.7	235	7	US-11-254-185-37	Sequence 37, Appl1
149	263	6.7	431	7	US-11-510-530-184	Sequence 184, App	225	224.5	5.7	235	7	US-11-253-869-5	Sequence 5, Appl1
150	262.5	6.7	461	6	US-10-219-051B-3545	Sequence 3545, Ap	226	224.5	5.7	235	7	US-11-253-869-37	Sequence 37, Appl1
151	262.5	6.7	461	7	US-11-435-001-3	Sequence 3, Appl1	227	224.5	5.7	272	7	US-11-327-490-40	Sequence 40, Appl1
152	262.5	6.7	1042	6	US-10-543-003-4	Sequence 4, Appl1	228	224	5.7	275	6	US-10-511-937-2457	Sequence 2457, Ap
153	261	6.6	431	6	US-10-219-051B-12109	Sequence 12109, A	229	224	5.7	275	6	US-10-530-798-22	Sequence 22, Appl1
154	258.5	6.6	412	7	US-11-444-594-2	Sequence 2, Appl1	230	224	5.7	275	7	US-11-327-490-36	Sequence 36, Appl1
155	258.5	6.6	412	7	US-10-652-846-11	Sequence 11, Appl	231	223.5	5.7	348	6	US-10-744-643-2421	Sequence 2421, Ap
156	255	6.5	263	6	US-10-294-433-417	Sequence 417, App	232	223.5	5.7	413	7	US-11-001-793-6341	Sequence 6341, Ap
157	253.5	6.5	487	6	US-10-533-520-3586	Sequence 3586, Ap	233	223.5	5.7	413	7	US-11-001-793-6341	Sequence 9519, App
158	252.5	6.4	314	6	US-10-495-479-4	Sequence 4, Appl1	234	223.5	5.7	457	7	US-11-371-354-70079	Sequence 70079, A
159	252.5	6.4	362	6	US-10-495-479-8	Sequence 8, Appl1	235	223.5	5.7	531	6	US-10-522-668-2	Sequence 2, Appl1
160	251.5	6.4	787	7	US-11-362-260A-342	Sequence 342, App	236	223.5	5.7	1203	7	US-11-090-997-930	Sequence 930, App
161	250.5	6.3	757	7	US-11-362-260A-345	Sequence 345, App	237	223	5.7	305	7	US-11-293-697-3002	Sequence 3002, Ap
162	249.5	6.3	875	6	US-10-570-909-19	Sequence 19, App	238	223	5.7	454	7	US-11-403-988-12	Sequence 12, Appl1
163	249.5	6.3	875	6	US-10-570-909-52	Sequence 52, Appl	239	222.5	5.6	790	7	US-11-314-939-13	Sequence 13, Appl1
164	248	6.3	230	7	US-11-254-185-8	Sequence 8, Appl1	240	222	5.6	275	6	US-10-530-798-23	Sequence 23, Appl1
165	248	6.3	230	7	US-11-254-185-40	Sequence 40, Appl1	241	222	5.6	275	6	US-10-530-798-25	Sequence 25, Appl1
166	248	6.3	230	7	US-11-253-869-8	Sequence 8, Appl1	242	222	5.6	275	6	US-10-219-051B-8826	Sequence 8826, Ap
167	248	6.3	230	7	US-11-253-869-40	Sequence 40, Appl	243	222	5.6	275	7	US-10-219-051B-8826	Sequence 8826, Ap
168	248	6.3	263	7	US-11-371-354-74719	Sequence 74719, A	244	222	5.6	422	7	US-11-371-354-63815	Sequence 63815, A
169	247	6.3	739	7	US-11-441-828-2	Sequence 2, Appl1	245	222	5.6	422	7	US-11-371-354-63815	Sequence 4722, App
170	247	6.3	764	6	US-10-529-348-2191	Sequence 2191, Ap	248	222	5.6	423	7	US-11-101-316-106	Sequence 106, App
171	247	6.3	764	7	US-11-371-354-73721	Sequence 73721, A	249	222	5.6	423	7	US-11-376-673-106	Sequence 106, App
172	247	6.3	764	7	US-11-441-828-1	Sequence 1, Appl1	250	222	5.6	423	7	US-11-265-767-146	Sequence 146, App
173	246.5	6.2	615	6	US-10-796-280-914	Sequence 914, App	251	222	5.6	428	7	US-11-102-284-106	Sequence 106, App
174	246.5	6.2	622	6	US-10-796-280-913	Sequence 913, App	252	222	5.6	428	7	US-11-510-530-218	Sequence 218, App
175	246.5	6.2	622	7	US-11-371-354-68137	Sequence 68137, A	255	221.5	5.6	453	6	US-10-245-882-206	Sequence 206, App
							256	221.5	5.6	453	7	US-11-403-988-2	Sequence 2, Appl1

257	221.5	5.6	2531	6	US-10-219-051B-9645	Sequence 9645, Ap	331	211	5.3	262	7	US-11-359-554-2	Sequence 2, Appli
258	221.5	5.6	2531	6	US-10-219-051B-9649	Sequence 9649, Ap	332	211	5.3	276	7	US-11-327-490-35	Sequence 35, Appl
259	221.5	5.6	2531	6	US-10-219-051B-9653	Sequence 9653, Ap	333	211	5.3	1067	7	US-11-054-369A-3	Sequence 3, Appl
260	221.5	5.6	2531	6	US-10-219-051B-9657	Sequence 9657, Ap	334	211	5.3	1218	6	US-10-833-833-14	Sequence 124, App
261	221	5.6	273	6	US-10-219-051B-8824	Sequence 8824, Ap	335	211	5.3	1218	6	US-10-219-051B-8286	Sequence 6286, Ap
262	221	5.6	273	6	US-10-219-051B-13255	Sequence 13255, A	336	211	5.3	1218	6	US-10-567-630-23	Sequence 23, Appl
263	221	5.6	273	6	US-10-219-051B-13259	Sequence 13259, A	337	211	5.3	1218	6	US-11-178-724-21	Sequence 21, Appl
264	221	5.6	1198	6	US-10-219-051B-4572	Sequence 4572, Ap	338	211	5.3	1218	7	US-11-071-796A-20	Sequence 20, Appl
265	220	5.6	275	6	US-10-530-798-24	Sequence 24, Appl	339	211	5.3	1218	7	US-11-188-417A-21	Sequence 21, Appl
266	220	5.6	275	6	US-10-530-798-26	Sequence 26, Appl	340	211	5.3	1218	7	US-11-231-494-21	Sequence 21, Appl
267	219.5	5.6	245	7	US-11-354-185-36	Sequence 36, Appl	341	210.5	5.3	339	7	US-11-404-745-2	Sequence 2, Appli
268	219.5	5.6	245	7	US-11-353-869-36	Sequence 36, Appl	342	210.5	5.3	505	7	US-11-293-697-3257	Sequence 3257, Ap
269	219.5	5.6	271	7	US-11-327-490-39	Sequence 39, Appl	343	210.5	5.3	572	6	US-10-760-320A-829	Sequence 4829, Ap
270	219.5	5.6	761	7	US-11-441-828-6	Sequence 6, Appli	344	210.5	5.3	1068	7	US-11-054-369A-1	Sequence 1, Appli
271	219	5.6	343	6	US-10-219-051B-13257	Sequence 13257, A	345	210.5	5.3	1219	6	US-10-219-051B-3232	Sequence 3232, Ap
272	219	5.6	343	6	US-10-219-051B-13261	Sequence 13261, A	346	210.5	5.3	1219	6	US-10-219-051B-6284	Sequence 6284, Ap
273	219	5.6	343	6	US-10-529-348-265	Sequence 265, App	347	209	5.3	307	6	US-11-066-316A-636	Sequence 636, App
274	219	5.6	343	7	US-11-359-554-3	Sequence 3, Appli	348	209	5.3	433	6	US-10-760-320A-4755	Sequence 4755, Ap
275	219	5.6	343	7	US-11-359-865-1	Sequence 1, Appli	349	209	5.3	492	5	US-10-669-920-454	Sequence 454, App
276	218.5	5.5	1201	7	US-11-371-354-70451	Sequence 70451, A	350	208.5	5.3	492	5	US-09-976-885-173	Sequence 173, App
277	218.5	5.5	1379	6	US-10-502-394-46	Sequence 932, App	351	208.5	5.3	492	7	US-11-344-933-895	Sequence 895, App
278	218.5	5.5	1379	6	US-11-327-490-3	Sequence 46, Appl	352	208.5	5.3	492	7	US-11-200-973-4	Sequence 94, Appl
279	218	5.5	268	6	US-10-405-027-3748	Sequence 3748, Ap	353	208.5	5.3	492	7	US-11-538-764-94	Sequence 173, App
280	217	5.5	268	6	US-11-371-354-57523	Sequence 57523, A	354	208.5	5.3	492	7	US-11-212-799-173	Sequence 10, Appl
281	217	5.5	284	6	US-10-405-027-4680	Sequence 4680, Ap	355	208	5.3	271	7	US-11-292-215-10	Sequence 74659, A
282	217	5.5	2703	6	US-10-781-059A-4	Sequence 4, Appli	356	207.5	5.3	269	7	US-11-371-354-74659	Sequence 74659, A
283	217	5.5	2703	6	US-11-359-554-6	Sequence 6, Appli	357	207.5	5.3	1047	7	US-11-288-992-12	Sequence 12, Appl
284	216	5.5	810	7	US-11-371-354-68191	Sequence 68191, A	358	207.5	5.3	1463	7	US-11-288-992-48	Sequence 48, Appl
285	216	5.5	810	7	US-11-353-972-1	Sequence 121, App	359	207	5.2	550	6	US-10-796-280-1057	Sequence 1057, Ap
286	216	5.5	1218	6	US-10-833-833-121	Sequence 121, App	360	206.5	5.2	250	7	US-11-478-144-657	Sequence 657, App
287	216	5.5	306	7	US-11-476-636-6	Sequence 263, App	361	206.5	5.2	272	7	US-11-327-490-37	Sequence 37, Appl
288	215.5	5.5	317	6	US-10-970-823-263	Sequence 263, App	362	206	5.2	275	7	US-11-319-952-72	Sequence 72, Appl
289	215.5	5.5	317	6	US-10-529-348-584	Sequence 584, App	363	206	5.2	426	6	US-10-760-320A-3218	Sequence 3218, Ap
290	215.5	5.5	317	6	US-11-476-636-2	Sequence 2, Appli	364	206	5.2	1169	6	US-10-796-280-841	Sequence 841, App
291	215.5	5.5	317	6	US-10-405-027-5294	Sequence 5294, Ap	365	206	5.2	269	7	US-11-371-354-70753	Sequence 166, App
292	215	5.5	268	6	US-10-777-288A-2471	Sequence 2471, Ap	366	205.5	5.2	492	7	US-11-344-933-932	Sequence 70753 A
293	215	5.5	790	7	US-11-350-703-1	Sequence 1, Appli	367	205.5	5.2	492	7	US-11-200-973-2	Sequence 932, App
294	215	5.5	791	7	US-11-318-939-6	Sequence 6, Appli	368	205.5	5.2	492	7	US-11-371-354-65497	Sequence 2, Appli
295	215	5.5	810	7	US-11-371-354-68531	Sequence 68531, A	369	205	5.2	492	7	US-11-344-933-934	Sequence 65497, A
296	215	5.5	1473	6	US-11-090-997-60	Sequence 4570, Ap	370	204.5	5.2	305	6	US-10-652-846-75	Sequence 934, App
297	214.5	5.4	1473	6	US-10-219-051B-4570	Sequence 4570, Ap	371	204.5	5.2	305	6	US-10-405-027-4807	Sequence 4807, Ap
298	214.5	5.4	275	6	US-10-219-051B-2020	Sequence 2020, Ap	372	204.5	5.2	305	6	US-10-405-027-4810	Sequence 4910, Ap
299	214.5	5.4	810	7	US-11-431-526-2	Sequence 2, Appli	373	204.5	5.2	305	6	US-10-219-051B-11184	Sequence 11184, A
300	214	5.4	810	7	US-11-354-185-6	Sequence 6, Appli	374	204.5	5.2	740	6	US-10-544-944-13	Sequence 12716, A
301	214	5.4	810	7	US-11-254-185-38	Sequence 38, Appl	375	204	5.2	260	6	US-10-652-846-7	Sequence 13, Appli
302	213.5	5.4	255	7	US-11-253-869-6	Sequence 38, Appl	376	204	5.2	260	6	US-10-529-348-608	Sequence 396, App
303	213.5	5.4	255	7	US-11-253-869-38	Sequence 38, Appl	377	204	5.2	260	6	US-10-529-348-608	Sequence 608, App
304	213.5	5.4	255	7	US-11-253-869-38	Sequence 38, Appl	378	204	5.2	260	6	US-11-319-952-83	Sequence 7, Appli
305	213.5	5.4	255	7	US-11-253-869-38	Sequence 38, Appl	379	204	5.2	260	6	US-11-295-040-7	Sequence 24, Appl
306	213.5	5.4	255	7	US-11-253-869-38	Sequence 38, Appl	380	204	5.2	260	6	US-11-254-185-7	Sequence 39, Appli
307	213.5	5.4	255	7	US-11-253-869-38	Sequence 38, Appl	381	204	5.2	260	6	US-11-254-185-7	Sequence 39, Appli
308	212.5	5.4	250	5	US-09-976-858-34	Sequence 34, Appl	382	204	5.2	260	6	US-11-254-185-7	Sequence 39, Appli
309	212.5	5.4	250	5	US-10-546-435-12	Sequence 12, Appl	383	203.5	5.2	224	7	US-11-253-869-7	Sequence 39, Appli
310	212.5	5.4	250	5	US-10-546-435-12	Sequence 12, Appl	384	203.5	5.2	224	7	US-11-253-869-7	Sequence 39, Appli
311	212.5	5.4	250	5	US-10-964-241-506	Sequence 506, App	385	203.5	5.2	224	7	US-11-253-869-7	Sequence 39, Appli
312	212.5	5.4	250	5	US-10-803-180-105	Sequence 106, App	386	203.5	5.2	224	7	US-11-253-869-7	Sequence 39, Appli
313	212.5	5.4	250	5	US-11-319-952-86	Sequence 86, App	387	203.5	5.2	224	7	US-11-253-869-7	Sequence 39, Appli
314	212.5	5.4	250	5	US-11-319-952-86	Sequence 86, App	388	203.5	5.2	224	7	US-11-253-869-7	Sequence 39, Appli
315	212.5	5.4	250	5	US-11-319-952-86	Sequence 86, App	389	203.5	5.2	224	7	US-11-253-869-7	Sequence 39, Appli
316	212.5	5.4	250	5	US-11-319-952-86	Sequence 86, App	390	203.5	5.2	224	7	US-11-253-869-7	Sequence 39, Appli
317	212.5	5.4	250	5	US-11-319-952-86	Sequence 86, App	391	203.5	5.2	224	7	US-11-253-869-7	Sequence 39, Appli
318	212.5	5.4	250	5	US-11-319-952-86	Sequence 86, App	392	203.5	5.2	224	7	US-11-253-869-7	Sequence 39, Appli
319	212.5	5.4	250	5	US-11-319-952-86	Sequence 86, App	393	203.5	5.2	224	7	US-11-253-869-7	Sequence 39, Appli
320	212.5	5.4	250	5	US-11-319-952-86	Sequence 86, App	394	203	5.1	185	6	US-10-527-191-1	Sequence 1, Appli
321	212.5	5.4	250	5	US-10-546-435-11	Sequence 11, Appl	395	203	5.1	581	6	US-10-574-786-2	Sequence 2, Appli
322	212.5	5.4	282	6	US-10-553-436-234	Sequence 234, App	396	202.5	5.1	228	7	US-11-319-952-73	Sequence 73, Appl
323	212.5	5.4	282	6	US-10-529-088-1	Sequence 107, App	397	202.5	5.1	239	7	US-11-371-354-61593	Sequence 61593, A
324	212.5	5.4	282	6	US-10-803-180-107	Sequence 107, App	398	202	5.1	200	6	US-10-533-519-674	Sequence 76749, A
325	212	5.4	260	7	US-10-652-846-8	Sequence 8, Appli	399	202	5.1	2321	6	US-10-518-751-8	Sequence 674, App
326	212	5.4	260	7	US-11-293-040-10	Sequence 10, Appl	400	202	5.1	2321	6	US-10-567-630-19	Sequence 19, Appl
327	211.5	5.4	235	7	US-11-254-185-4	Sequence 4, Appli	401	201.5	5.1	256	6	US-10-529-163-7	Sequence 7, Appli
328	211.5	5.4	235	7	US-11-253-869-4	Sequence 4, Appli	402	201.5	5.1	256	6	US-11-066-316A-635	Sequence 635, App
329	211.5	5.4	418	6	US-10-529-348-693	Sequence 693, App	403	201.5	5.1	438	6	US-10-760-320A-2876	Sequence 2876, Ap
330	211.5	5.4	418	7	US-11-371-354-69437	Sequence 69437, A	404	201	5.1	1054	7	US-11-288-992-47	Sequence 47, Appl

405	200.5	5.1	185	6	US-10-527-191-12	Sequence 12, Appl	479	189	4.8	253	6	US-10-544-944-10	Sequence 10, Appl
406	200.5	5.1	185	7	US-11-371-354-68349	Sequence 68349, A	480	189	4.8	253	6	US-10-529-348-576	Sequence 576, App
407	200.5	5.1	415	6	US-10-970-823-104	Sequence 104, App	481	189	4.8	253	7	US-11-371-354-62399	Sequence 62399, A
408	200.5	5.1	752	7	US-11-371-354-64631	Sequence 64631, A	482	189	4.8	253	7	US-11-538-764-95	Sequence 95, Appl
409	200.5	5.1	810	7	US-11-318-939-11	Sequence 11, Appl	483	189	4.8	449	7	US-11-344-932-617	Sequence 617, App
410	200	5.1	385	7	US-11-371-354-62531	Sequence 62531, A	484	189	4.8	585	7	US-11-344-932-1020	Sequence 1020, Ap
411	199.5	5.1	348	7	US-11-371-354-65083	Sequence 65083, A	485	189	4.8	1176	7	US-11-090-997-1018	Sequence 1018, Ap
412	199.5	5.1	2556	6	US-10-781-059A-2	Sequence 2, Appl1	486	188.5	4.8	282	6	US-10-219-051B-13543	Sequence 3543, Ap
413	199.5	5.1	2556	7	US-11-071-796A-22	Sequence 22, Appl	488	188.5	4.8	290	6	US-10-964-241-222	Sequence 222, App
414	198.5	5.0	170	6	US-10-537-507A-2	Sequence 2, Appl1	489	188.5	4.8	290	6	US-10-529-348-1862	Sequence 1862, Ap
415	198.5	5.0	223	7	US-11-258-174-14	Sequence 14, Appl	490	188.5	4.8	280	7	US-11-001-793-908	Sequence 908, Ap
416	198.5	5.0	311	7	US-11-359-858-2	Sequence 2, Appl1	491	188.5	4.8	2451	6	US-10-669-920-908	Sequence 908, App
417	198.5	5.0	790	7	US-11-066-316A-1092	Sequence 1092, Ap	492	188.5	4.8	2503	6	US-10-539-228-723	Sequence 723, App
418	198.5	5.0	830	7	US-11-066-316A-1093	Sequence 1093, Ap	493	188	4.8	228	7	US-11-478-089-2	Sequence 2, Appl1
419	198.5	5.0	830	7	US-11-066-316A-1094	Sequence 1094, Ap	494	188	4.8	249	7	US-11-119-952-68	Sequence 68, Appl
420	198	5.0	235	6	US-10-530-798-1	Sequence 1, Appl1	495	188	4.8	253	6	US-10-219-051B-4094	Sequence 4094, Ap
421	198	5.0	235	7	US-11-430-214-72	Sequence 72, Appl	496	188	4.8	254	7	US-11-344-932-523	Sequence 523, Appl
423	198	5.0	1023	6	US-10-964-241-200	Sequence 200, App	497	188	4.8	288	6	US-10-530-643-22	Sequence 22, Appl
424	197.5	5.0	248	6	US-10-529-163-2	Sequence 2, Appl1	498	188	4.8	311	7	US-11-327-490-41	Sequence 41, Appl
425	197.5	5.0	248	7	US-11-319-952-60	Sequence 60, Appl	499	188	4.8	333	7	US-11-318-939-8	Sequence 8, Appl1
426	197.5	5.0	269	7	US-11-246-999-127	Sequence 127, App	500	187.5	4.8	224	7	US-11-441-635-8	Sequence 7, Appl1
427	197.5	5.0	2494	6	US-10-669-920-22	Sequence 22, Appl	501	187.5	4.8	227	6	US-10-441-635-691	Sequence 691, App
428	197	5.0	235	6	US-10-530-798-2	Sequence 2, Appl1	502	187.5	4.8	247	7	US-11-371-354-70767	Sequence 70767, A
429	197	5.0	338	7	US-11-318-939-10	Sequence 10, Appl	503	187.5	4.8	252	6	US-10-703-032-122453	Sequence 122453, A
430	196.5	5.0	1052	7	US-11-218-141-1000	Sequence 1000, Ap	504	187.5	4.8	932	7	US-11-090-997-1878	Sequence 1878, Ap
431	196.5	5.0	2523	6	US-10-781-059A-3	Sequence 3, Appl1	505	187.5	4.8	932	7	US-11-090-997-1874	Sequence 1874, Ap
432	196	5.0	270	7	US-11-371-354-74827	Sequence 74827, A	506	187.5	4.8	1008	7	US-11-288-992-11	Sequence 11, Appl
433	195.5	5.0	257	7	US-11-371-354-57395	Sequence 57395, A	507	187	4.7	281	7	US-11-293-697-2976	Sequence 2976, Ap
434	195.5	5.0	257	7	US-11-127-581-8	Sequence 8, Appl1	508	187	4.7	226	7	US-11-319-952-22	Sequence 22, Appl
435	195.5	5.0	2000	6	US-10-533-519-512	Sequence 512, App	509	186	4.7	1176	6	US-10-777-288A-2974	Sequence 2974, Appl
436	195.5	5.0	2471	6	US-10-781-059A-1	Sequence 1, Appl1	510	185.5	4.7	711	7	US-11-478-193-1080	Sequence 1080, Ap
437	195.5	5.0	2471	6	US-10-219-051B-4116	Sequence 4116, Ap	511	185.5	4.7	713	7	US-11-175-714-5	Sequence 5, Appl1
438	195.5	5.0	2471	6	US-10-219-051B-9647	Sequence 9647, Ap	512	185.5	4.7	725	6	US-10-990-328-10445	Sequence 10445, A
439	195.5	5.0	2471	6	US-10-219-051B-9651	Sequence 9651, Ap	513	184.5	4.7	601	7	US-11-090-997-1876	Sequence 1876, Ap
440	195.5	5.0	2471	6	US-10-219-051B-9655	Sequence 9655, Ap	514	184.5	4.7	917	7	US-11-090-997-1872	Sequence 1872, Ap
441	195.5	5.0	2471	6	US-10-219-051B-9659	Sequence 9659, Ap	515	184	4.7	144	6	US-10-652-846-1	Sequence 1, Appl1
442	195.5	5.0	2471	6	US-10-567-630-17	Sequence 17, Appl	516	184	4.7	144	6	US-11-295-040-1	Sequence 257, App
443	195.5	5.0	2471	7	US-11-071-796A-23	Sequence 23, Appl	517	184	4.7	314	6	US-10-970-823-257	Sequence 257, App
444	195	4.9	258	7	US-11-319-952-85	Sequence 85, Appl	518	184	4.7	314	6	US-10-105-299-5979	Sequence 5979, App
445	195	4.9	432	6	US-10-219-051B-12107	Sequence 12107, A	519	184	4.7	314	6	US-10-868-184-4975	Sequence 4975, Ap
446	194	4.9	113	7	US-11-254-185-26	Sequence 26, Appl	520	183.5	4.6	721	6	US-10-594-608-5979	Sequence 5979, Ap
447	194	4.9	113	7	US-11-253-869-56	Sequence 26, Appl	521	183.5	4.6	251	6	US-10-576-491-2	Sequence 2, Appl1
448	194	4.9	113	7	US-11-507-474-20	Sequence 20, Appl	522	183.5	4.6	768	7	US-11-066-316A-1091	Sequence 1091, Ap
449	194	4.9	233	4	US-11-478-089-4	Sequence 4, Appl1	523	182.5	4.6	157	6	US-10-760-320A-3310	Sequence 3310, Ap
450	194	4.9	637	6	US-10-990-920-451	Sequence 10446, A	524	182.5	4.6	260	7	US-11-429-599-21	Sequence 21, Appl
451	194	4.9	3609	6	US-10-669-920-651	Sequence 451, App	525	182.5	4.6	468	6	US-10-743-643-1064	Sequence 1064, Appl
452	193.5	4.9	347	6	US-10-743-643-2419	Sequence 2419, Ap	526	182.5	4.6	720	7	US-11-175-714-4	Sequence 4, Appl1
453	193.5	4.9	2471	6	US-10-219-051B-4114	Sequence 4114, Ap	527	182	4.6	421	6	US-10-760-320A-4767	Sequence 4767, Ap
454	193	4.9	228	6	US-10-533-519-1031	Sequence 1031, Ap	528	182	4.6	721	7	US-11-175-714-7	Sequence 7, Appl1
455	193	4.9	228	6	US-10-529-348-528	Sequence 528, App	529	182	4.6	1057	7	US-11-054-369A-5	Sequence 5, Appl1
456	193	4.9	228	6	US-10-533-530-6140	Sequence 6140, Ap	530	182	4.6	1159	6	US-10-540-844-4	Sequence 4, Appl1
457	193	4.9	253	7	US-11-319-952-59	Sequence 69, Appl	531	182	4.6	1256	6	US-10-540-844-2	Sequence 2, Appl1
458	192.5	4.9	194	6	US-10-530-798-21	Sequence 21, Appl	532	182	4.6	1238	6	US-10-219-051B-3334	Sequence 3334, Ap
459	192.5	4.9	226	6	US-10-530-798-3	Sequence 3, Appl1	533	182	4.6	1238	6	US-10-219-051B-6747	Sequence 6747, Ap
460	192.5	4.9	247	6	US-10-529-348-1120	Sequence 1120, Ap	534	182	4.6	1238	6	US-10-567-630-35	Sequence 35, Appl
461	192.5	4.9	281	7	US-11-292-215-7	Sequence 7, Appl1	535	182	4.6	1238	6	US-10-567-630-35	Sequence 35, Appl
462	192	4.9	149	7	US-11-400-825-20	Sequence 20, Appl	536	182	4.6	1238	6	US-10-529-348-10	Sequence 10, Appl
463	191.5	4.9	224	7	US-11-441-635-5	Sequence 5, Appl1	537	182	4.6	1238	7	US-11-178-124-22	Sequence 22, Appl
464	191.5	4.9	246	6	US-10-547-510-54	Sequence 54, Appl	538	182	4.6	1238	7	US-11-071-796A-21	Sequence 21, Appl
465	191.5	4.9	247	7	US-11-319-952-82	Sequence 82, Appl	539	182	4.6	1238	7	US-11-188-417A-22	Sequence 22, Appl
466	191.5	4.9	579	7	US-11-166-372-1884	Sequence 1884, Ap	540	182	4.6	1238	7	US-11-188-417A-22	Sequence 22, Appl
467	191.5	4.9	830	6	US-10-505-928-469	Sequence 469, App	541	181.5	4.6	823	7	US-11-231-694-22	Sequence 82, Appl
468	191	4.8	226	7	US-11-403-988-5	Sequence 5, Appl1	542	181.5	4.6	823	7	US-11-390-921-5	Sequence 8, Appl1
469	191	4.8	228	7	US-11-371-354-68221	Sequence 68221, A	543	181.5	4.6	876	7	US-11-090-997-1882	Sequence 1882, Ap
470	191	4.8	254	7	US-11-319-952-3	Sequence 3, Appl1	544	181	4.6	876	7	US-11-090-997-1880	Sequence 1880, Ap
471	191	4.8	254	7	US-11-339-723-50	Sequence 50, Appl	545	181	4.6	257	7	US-11-319-952-87	Sequence 87, Appl
472	191	4.8	254	7	US-11-344-932-525	Sequence 525, App	546	181	4.6	831	7	US-11-218-141-3868	Sequence 3868, Ap
473	190.5	4.8	251	7	US-11-319-952-77	Sequence 77, Appl	547	181	4.6	862	7	US-11-218-141-1769	Sequence 1769, App
474	190	4.8	253	6	US-10-574-398-70	Sequence 70, Appl	548	181	4.6	862	7	US-11-218-141-37378	Sequence 3737, Ap
475	190	4.8	253	7	US-11-441-828-7	Sequence 7, Appl1	549	181	4.6	910	6	US-10-964-141-112	Sequence 112, App
476	190	4.8	254	7	US-11-319-952-51	Sequence 81, Appl	550	181	4.6	254	6	US-10-529-163-1	Sequence 1, Appl1
477	189	4.8	220	7	US-11-344-932-327	Sequence 327, App	551	180	4.6	254	7	US-11-319-952-59	Sequence 59, Appl
478	189	4.8	237	7	US-11-319-952-2	Sequence 2, Appl1	552	180	4.6	2087	6	US-10-669-920-911	Sequence 911, App

554	180	4.6	2087	6	US-10-669-920-913	Sequence 913, App	627	171.5	4.3	2403	6	US-10-527-191-88	Sequence 88, Appl
555	180	4.6	2203	7	US-10-539-228-726	Sequence 726, App	628	171.5	4.3	2413	6	US-10-511-937-2616	Sequence 2616, Ap
556	179.5	4.6	205	7	US-11-349-541-176	Sequence 176, App	629	171.5	4.3	2413	6	US-10-527-191-89	Sequence 89, Appl
557	179.5	4.6	205	7	US-11-944-932-117	Sequence 176, App	630	171.5	4.3	2413	6	US-10-527-191-106	Sequence 106, App
558	179.5	4.6	250	6	US-10-529-348-1910	Sequence 1910, Ap	631	171	4.3	256	7	US-11-319-952-44	Sequence 44, Appl
559	179.5	4.6	250	7	US-11-319-952-23	Sequence 23, Appl	632	171	4.3	258	7	US-11-158-252-63	Sequence 63, Appl
560	178	4.5	556	6	US-10-796-280-915	Sequence 915, App	633	171	4.3	277	6	US-10-526-111-1	Sequence 1, Appl1
561	178	4.5	996	7	US-11-538-764-151	Sequence 151, App	634	171	4.3	277	6	US-10-529-348-578	Sequence 578, App
562	177.5	4.5	249	6	US-10-743-643-116	Sequence 116, App	635	171	4.3	277	6	US-11-319-952-45	Sequence 45, App
563	177.5	4.5	271	7	US-11-429-599-23	Sequence 23, Appl	636	171	4.3	277	7	US-11-371-354-70755	Sequence 70755, A
564	177	4.5	112	7	US-11-254-185-27	Sequence 27, Appl	637	171	4.3	277	7	US-11-436-059-8	Sequence 8, Appl1
565	177	4.5	112	7	US-11-253-869-27	Sequence 27, Appl	640	171	4.3	737	7	US-11-296-092-15	Sequence 15, Appl
566	177	4.5	729	7	US-11-175-714-8	Sequence 8, Appl1	641	171	4.3	737	7	US-11-296-155-15	Sequence 15, Appl
567	177	4.5	1088	6	US-10-669-920-1337	Sequence 1337, Ap	642	171	4.3	777	7	US-11-218-141-1900	Sequence 1900, Ap
568	177	4.5	1200	6	US-10-567-630-27	Sequence 27, Appl	643	171	4.3	2412	6	US-10-527-191-70	Sequence 70, Appl
569	177	4.5	1200	6	US-10-743-643-979	Sequence 979, App	644	171	4.3	2412	6	US-10-527-191-105	Sequence 105, Appl
570	176.5	4.5	2002	6	US-10-567-630-21	Sequence 21, Appl	645	171	4.3	2413	6	US-10-219-051B-8374	Sequence 8374, Ap
571	176.5	4.5	2003	6	US-10-767-471-911	Sequence 911, App	646	171	4.3	2413	6	US-10-219-051B-8378	Sequence 8378, Ap
572	176.5	4.5	2003	6	US-10-767-471-932	Sequence 932, App	647	171	4.3	2413	6	US-10-219-051B-11886	Sequence 11886, A
573	176.5	4.5	2003	6	US-10-990-328-10382	Sequence 10382, A	648	170	4.3	864	7	US-11-178-724-27	Sequence 27, Appl
574	176.5	4.5	2003	6	US-10-990-328-10403	Sequence 10403, A	649	170	4.3	864	7	US-11-188-417A-98	Sequence 98, Appl
575	176.5	4.5	2003	7	US-11-264-243-8	Sequence 8, Appl1	650	170	4.3	864	7	US-11-231-494-34	Sequence 34, Appl
576	176	4.5	270	7	US-11-371-354-74657	Sequence 74657, A	651	169.5	4.3	542	7	US-11-054-369A-7	Sequence 7, Appl1
577	176	4.5	270	7	US-11-371-354-74763	Sequence 74763, A	652	169.5	4.3	723	6	US-10-567-630-29	Sequence 29, Appl
578	175	4.4	112	7	US-11-507-474-21	Sequence 21, Appl	653	169	4.3	2067	6	US-10-669-920-1343	Sequence 1343, Ap
579	175	4.4	464	7	US-11-001-793-8731	Sequence 8731, Ap	654	168	4.3	609	7	US-11-090-997-1904	Sequence 1904, Ap
580	175	4.4	487	6	US-10-105-299-6146	Sequence 6146, Ap	655	168	4.3	644	6	US-10-508-580-16	Sequence 16, Appl
581	175	4.4	487	6	US-10-868-184-5142	Sequence 5142, Ap	656	168	4.3	644	6	US-10-508-580-16	Sequence 4382, Ap
582	175	4.4	487	6	US-10-994-608-6146	Sequence 6146, Ap	657	168	4.3	698	6	US-10-405-027-3107	Sequence 3107, Ap
583	175	4.4	555	6	US-10-405-027-5382	Sequence 5382, Ap	658	168	4.3	923	6	US-10-533-519-1684	Sequence 1684, Ap
584	175	4.4	555	6	US-10-796-280-707	Sequence 707, App	659	168	4.3	923	7	US-11-090-997-1992	Sequence 1902, Ap
585	175	4.4	555	7	US-11-066-316A-586	Sequence 586, App	660	168	4.3	923	7	US-11-488-364-2	Sequence 2, Appl1
586	175	4.4	901	6	US-10-796-280-708	Sequence 708, App	661	167.5	4.2	255	7	US-11-319-952-74	Sequence 74, Appl1
587	175	4.4	901	6	US-11-066-316A-585	Sequence 585, App	662	167.5	4.2	256	7	US-11-319-952-76	Sequence 76, Appl
588	175	4.4	909	6	US-10-796-280-704	Sequence 704, App	663	167.5	4.2	261	6	US-10-652-846-10	Sequence 10, Appl
589	175	4.4	909	6	US-11-066-316A-588	Sequence 588, App	664	167.5	4.2	261	7	US-11-319-952-78	Sequence 78, Appl
590	175	4.4	926	6	US-10-533-519-1635	Sequence 1635, Ap	665	167.5	4.2	261	7	US-11-323-964-10	Sequence 10, Appl
591	175	4.4	926	6	US-10-796-280-706	Sequence 706, App	666	167.5	4.2	261	7	US-11-430-214-70	Sequence 70, Appl
592	175	4.4	926	7	US-11-066-316A-583	Sequence 583, App	667	167.5	4.2	261	7	US-11-430-214-75	Sequence 75, Appl
593	175	4.4	926	7	US-11-488-364-4	Sequence 4, Appl1	668	167.5	4.2	261	7	US-11-371-354-74655	Sequence 74655, A
594	175	4.4	969	6	US-10-796-280-710	Sequence 710, App	669	167.5	4.2	262	6	US-10-803-180-105	Sequence 105, App
595	175	4.4	969	6	US-11-066-316A-584	Sequence 584, App	670	167.5	4.2	262	6	US-11-319-952-80	Sequence 80, Appl
596	175	4.4	1080	6	US-10-767-471-934	Sequence 934, App	671	167.5	4.2	262	7	US-11-066-316A-974	Sequence 974, App
597	175	4.4	1080	6	US-10-990-328-10398	Sequence 10398, A	672	167.5	4.2	262	6	US-10-570-909-118	Sequence 118, App
598	175	4.4	1080	6	US-10-990-328-10405	Sequence 10405, A	673	167	4.2	222	6	US-10-553-436-293	Sequence 293, App
599	175	4.4	1080	6	US-11-362-260A-346	Sequence 346, App	674	166.5	4.2	262	7	US-11-371-354-74963	Sequence 74963, A
600	174.5	4.4	544	6	US-10-538-197-26	Sequence 26, Appl	676	166.5	4.2	723	6	US-10-964-241-346	Sequence 346, App
601	174.5	4.4	258	6	US-10-449-902-31884	Sequence 31884, A	677	166.5	4.2	723	7	US-11-178-724-18	Sequence 18, Appl
602	174	4.4	286	7	US-11-292-215-9	Sequence 9, Appl1	678	166.5	4.2	723	7	US-11-071-796A-17	Sequence 17, Appl
603	174	4.4	808	6	US-10-796-280-709	Sequence 709, App	679	166.5	4.2	723	7	US-11-188-417A-18	Sequence 18, Appl
604	174	4.4	808	6	US-11-066-316A-587	Sequence 587, App	680	166.5	4.2	723	7	US-11-231-494-18	Sequence 18, Appl
605	174	4.4	808	6	US-11-066-316A-587	Sequence 587, App	681	166.5	4.2	723	7	US-11-231-494-18	Sequence 18, Appl
606	174	4.4	931	7	US-11-343-271-40	Sequence 40, Appl	682	166	4.2	300	7	US-11-371-354-55701	Sequence 55701, A
607	173.5	4.4	294	6	US-10-105-299-4807	Sequence 4807, Ap	683	166	4.2	923	6	US-10-533-519-1576	Sequence 1576, Ap
608	173.5	4.4	294	6	US-10-868-184-3803	Sequence 3803, Ap	684	165.5	4.2	383	7	US-11-371-354-73975	Sequence 73975, A
609	173.5	4.4	294	6	US-10-994-608-4807	Sequence 4807, Ap	685	165.5	4.2	698	7	US-11-066-316A-594	Sequence 594, App
610	173.5	4.4	717	7	US-11-175-714-9	Sequence 9, Appl1	687	164.5	4.2	241	6	US-10-964-241-248	Sequence 248, App
611	173.5	4.4	809	7	US-11-371-354-71581	Sequence 71581, A	688	164.5	4.2	241	7	US-11-371-354-65937	Sequence 65937, A
612	173.5	4.4	853	7	US-11-218-141-1770	Sequence 1770, Ap	689	164.5	4.2	249	6	US-10-219-051B-14650	Sequence 14650, A
613	173	4.4	248	6	US-10-743-643-1289	Sequence 1289, Ap	690	164.5	4.2	329	7	US-11-345-903-11	Sequence 11, Appl
614	173	4.4	270	7	US-11-371-354-75053	Sequence 75053, A	691	164.5	4.2	449	7	US-11-371-354-65387	Sequence 65387, A
615	173	4.4	302	7	US-11-476-636-18	Sequence 18, Appl	692	164.5	4.2	449	7	US-11-354-559-4	Sequence 4, Appl1
616	173	4.4	701	7	US-11-362-260A-343	Sequence 343, App	693	164.5	4.2	449	7	US-11-354-559-6	Sequence 6, Appl1
617	173	4.4	768	6	US-10-219-051B-12714	Sequence 12714, A	694	164.5	4.2	1168	6	US-10-796-307-885	Sequence 885, App
618	172.5	4.4	449	6	US-10-743-643-1066	Sequence 1066, Ap	695	164.5	4.2	1172	6	US-10-796-307-887	Sequence 887, App
619	172.5	4.4	449	6	US-11-371-354-71577	Sequence 71577, A	696	164.5	4.2	1231	6	US-10-796-307-888	Sequence 888, App
620	172.5	4.4	567	6	US-10-538-197-22	Sequence 22, Appl	697	164.5	4.2	1231	6	US-10-796-307-888	Sequence 888, App
621	172.5	4.4	1208	6	US-10-219-051B-6745	Sequence 6745, Ap	698	164.5	4.2	1231	6	US-10-796-307-888	Sequence 888, App
622	172	4.4	1208	7	US-11-090-997-6	Sequence 6, Appl1	699	164.5	4.2	1231	6	US-11-354-559-2	Sequence 2, Appl1
623	171.5	4.3	262	6	US-10-652-846-9	Sequence 9, Appl1	700	164.5	4.2	1231	7	US-11-354-559-5	Sequence 5, Appl1
624	171.5	4.3	262	6	US-11-196-627-1021	Sequence 1021, Ap	701	164.5	4.2	1231	7	US-11-354-559-337	Sequence 337, App
625	171.5	4.3	1785	6	US-10-527-191-90	Sequence 90, Appl	702	164	4.2	484	7	US-11-231-494-56	Sequence 56, Appl
626	171.5	4.3	1785	7	US-11-510-493-5	Sequence 5, Appl1	703	163.5	4.1	859	6	US-10-533-519-1242	Sequence 1242, Ap

704	163.5	4.1	850	6	US-10-533-519-2355	Sequence 2255, Ap	781	156	4.0	866	6	US-10-669-920-1339	Sequence 1339, Ap
705	163.5	4.1	859	7	US-11-371-354-63565	Sequence 63565, A	782	155.5	3.9	830	7	US-11-175-714-11	Sequence 11, Appl
706	163	4.1	262	7	US-11-415-342-24	Sequence 24, Appl	783	155	3.9	243	6	US-10-553-869-1	Sequence 1, Appl1
707	163	4.1	315	6	US-10-664-356-1774	Sequence 1774, Ap	784	155	3.9	2039	6	US-10-219-051B-3230	Sequence 3230, Ap
708	163	4.1	315	7	US-11-001-793-9386	Sequence 9386, Ap	785	155	3.9	2489	7	US-11-429-673-5	Sequence 5, Appl1
709	163	4.1	600	6	US-10-664-356-1389	Sequence 1389, Ap	786	154.5	3.9	239	7	US-11-258-174-15	Sequence 15, Appl
710	163	4.1	600	7	US-11-001-793-6128	Sequence 6128, Ap	787	154.5	3.9	264	7	US-11-247-886-1	Sequence 1, Appl1
711	163	4.1	607	6	US-10-970-823-150	Sequence 150, App	788	154	3.9	246	7	US-11-247-886-2	Sequence 2, Appl1
712	163	4.1	607	6	US-10-964-241-344	Sequence 344, App	789	154	3.9	247	7	US-11-415-342-16	Sequence 16, Appl1
713	162.5	4.1	261	7	US-11-430-214-89	Sequence 89, Appl	790	154	3.9	248	6	US-10-219-051B-14652	Sequence 14652, Ap
714	162.5	4.1	1291	6	US-10-219-051B-8372	Sequence 8372, Ap	791	154	3.9	329	6	US-10-527-191-31	Sequence 31, Appl1
715	162.5	4.1	1291	6	US-10-219-051B-8376	Sequence 8376, Ap	792	154	3.9	1931	7	US-11-173-310-3	Sequence 3, Appl1
716	162.5	4.1	1291	6	US-10-219-051B-1884	Sequence 1884, A	793	154	3.9	1998	7	US-11-173-310-2	Sequence 2, Appl1
717	162.5	4.1	1291	6	US-10-449-902-40162	Sequence 40162, A	794	154	3.9	2039	6	US-10-219-051B-2028	Sequence 2028, Ap
718	162	4.1	248	6	US-11-457-438-2	Sequence 2, Appl1	795	154	3.9	2039	6	US-10-219-051B-2032	Sequence 2032, Ap
719	161.5	4.1	260	7	US-10-544-944-3	Sequence 3, Appl1	796	153.5	3.9	260	6	US-10-219-051B-8828	Sequence 8828, Ap
720	161	4.1	293	6	US-10-546-435-1	Sequence 1, Appl1	797	153.5	3.9	610	5	US-09-976-858-236	Sequence 236, App
721	161	4.1	293	6	US-10-664-356-1208	Sequence 1208, Ap	798	153.5	3.9	610	6	US-10-505-928-580	Sequence 580, App
722	161	4.1	293	6	US-10-664-356-1688	Sequence 1688, Ap	799	153.5	3.9	610	7	US-11-212-799-32	Sequence 236, App
723	161	4.1	293	6	US-10-664-356-1590	Sequence 1590, Ap	800	153.5	3.9	648	7	US-11-127-581-12	Sequence 12, Appl
724	161	4.1	293	6	US-10-664-356-1590	Sequence 1591, Ap	801	153	3.9	90	6	US-10-276-8170-15553	Sequence 15573, A
725	161	4.1	293	6	US-10-664-356-1591	Sequence 456, App	802	153	3.9	156	6	US-10-528-2608-246	Sequence 246, App
726	161	4.1	293	6	US-10-964-241-456	Sequence 14, Appl	803	153	3.9	243	6	US-10-553-869-7	Sequence 4, Appl1
727	161	4.1	293	7	US-11-319-952-14	Sequence 73575, A	804	153	3.9	243	6	US-10-553-869-4	Sequence 7, Appl1
728	161	4.1	293	7	US-11-371-354-73575	Sequence 2, Appl1	805	153	3.9	244	7	US-11-247-886-6	Sequence 6, Appl1
729	161	4.1	293	7	US-11-436-059-2	Sequence 5924, Ap	806	153	3.9	868	6	US-10-796-280-1062	Sequence 1062, Ap
730	161	4.1	293	7	US-11-001-793-5924	Sequence 9286, Ap	807	153	3.9	227	7	US-10-796-307-651	Sequence 651, App
731	161	4.1	293	7	US-11-001-793-9286	Sequence 9288, A	808	152.5	3.9	264	6	US-10-425-882-266	Sequence 266, App
732	161	4.1	293	7	US-11-001-793-9286	Sequence 9289, Ap	809	152.5	3.9	264	6	US-10-533-520-1797	Sequence 1797, Ap
733	161	4.1	293	7	US-11-001-793-9288	Sequence 28, Appl	810	152.5	3.9	264	6	US-10-533-520-1797	Sequence 1797, Ap
734	161	4.1	293	7	US-11-001-793-9289	Sequence 54, Appl	811	152.5	3.9	264	6	US-10-533-520-6168	Sequence 6168, Ap
735	160	4.1	113	7	US-11-254-185-28	Sequence 28, Appl	812	152.5	3.9	264	7	US-11-255-634-1	Sequence 1, Appl1
736	160	4.1	113	7	US-11-253-868-28	Sequence 54, Appl	813	152.5	3.9	264	7	US-11-466-321-26	Sequence 26, Appl1
737	160	4.1	207	6	US-10-154-678-54	Sequence 54, Appl	814	152.5	3.9	264	7	US-11-371-354-64269	Sequence 64269, A
738	160	4.1	207	6	US-10-154-678-54	Sequence 57, Appl	815	152.5	3.9	264	7	US-11-478-193-404	Sequence 404, App
739	160	4.1	227	6	US-11-412-325-54	Sequence 57, Appl	816	152.5	3.9	400	6	US-10-796-280-1194	Sequence 1194, App
740	160	4.1	227	6	US-10-553-869-57	Sequence 57, Appl	817	152.5	3.9	400	6	US-11-371-354-68361	Sequence 68361, A
741	160	4.1	227	6	US-10-553-869-57	Sequence 57, Appl	818	152.5	3.9	422	6	US-10-796-280-1196	Sequence 1196, Ap
742	160	4.1	227	6	US-10-553-869-57	Sequence 57, Appl	819	152.5	3.9	513	7	US-11-214-0634-1308	Sequence 1308, Ap
743	160	4.1	227	6	US-10-553-869-57	Sequence 57, Appl	820	152.5	3.9	642	7	US-11-153-714-10	Sequence 10, Appl
744	160	4.1	227	6	US-10-553-869-57	Sequence 57, Appl	821	152.5	3.9	243	6	US-10-553-869-2	Sequence 2, Appl1
745	160	4.1	227	6	US-10-553-869-57	Sequence 57, Appl	822	152	3.9	243	6	US-10-553-869-3	Sequence 3, Appl1
746	160	4.1	227	6	US-10-553-869-57	Sequence 57, Appl	823	152	3.9	243	6	US-10-553-869-4	Sequence 4, Appl1
747	160	4.1	227	6	US-10-553-869-57	Sequence 57, Appl	824	152	3.9	243	6	US-10-553-869-5	Sequence 5, Appl1
748	160	4.1	227	6	US-10-553-869-57	Sequence 57, Appl	825	152	3.9	243	6	US-10-553-869-6	Sequence 6, Appl1
749	160	4.1	227	6	US-10-553-869-57	Sequence 57, Appl	826	152	3.9	243	6	US-10-553-869-7	Sequence 7, Appl1
750	159.5	4.0	287	6	US-10-405-027-3719	Sequence 70, Appl	827	152	3.9	247	6	US-10-511-937-22472	Sequence 22472
751	159	4.0	287	6	US-11-319-952-70	Sequence 70, Appl	828	152	3.9	247	6	US-10-511-937-22472	Sequence 22472
752	159	4.0	287	6	US-11-319-952-70	Sequence 70, Appl	829	152	3.9	247	6	US-10-511-937-22472	Sequence 22472
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754	159	4.0	287	6	US-11-319-952-70	Sequence 70, Appl	831	152	3.9	247	6	US-10-511-937-22472	Sequence 22472
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756	159	4.0	287	6	US-11-319-952-70	Sequence 70, Appl	833	152	3.9	247	6	US-10-511-937-22472	Sequence 22472
757	159	4.0	287	6	US-11-319-952-70	Sequence 70, Appl	834	152	3.9	247	6	US-10-511-937-22472	Sequence 22472
758	159	4.0	287	6	US-11-319-952-70	Sequence 70, Appl	835	152	3.9	247	6	US-10-511-937-22472	Sequence 22472
759	159	4.0	287	6	US-11-319-952-70	Sequence 70, Appl	836	152	3.9	247	6	US-10-511-937-22472	Sequence 22472
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765	158.5	4.0	283	7	US-11-357-337-2	Sequence 144, App	842	152	3.9	281	6	US-10-796-280-11338	Sequence 11338
766	158	4.0	211	6	US-10-760-320A-4851	Sequence 4851, Ap	843	152	3.9	353	7	US-11-415-342-57	Sequence 57, Appl
767	158	4.0	211	6	US-10-760-320A-4851	Sequence 4851, Ap	844	152	3.9	353	7	US-11-415-342-57	Sequence 57, Appl
768	158	4.0	211	6	US-10-760-320A-4851	Sequence 4851, Ap	845	152	3.9	353	7	US-11-415-342-57	Sequence 57, Appl
769	158	4.0	211	6	US-10-760-320A-4851	Sequence 4851, Ap	846	151.5	3.8	251	7	US-11-371-354-74899	Sequence 74899, A
770	158	4.0	211	6	US-10-760-320A-4851	Sequence 4851, Ap	847	151.5	3.8	277	7	US-10-245-882-213	Sequence 213, App
771	158	4.0	211	6	US-10-760-320A-4851	Sequence 4851, Ap	848	151.5	3.8	277	7	US-10-245-882-213	Sequence 213, App
772	158	4.0	211	6	US-10-760-320A-4851	Sequence 4851, Ap	849	151.5	3.8	277	7	US-10-245-882-213	Sequence 213, App
773	158	4.0	211	6	US-10-760-320A-4851	Sequence 4851, Ap	850	151.5	3.8	277	7	US-10-245-882-213	Sequence 213, App
774	157.5	4.0	383	7	US-11-090-997-1040	Sequence 1040, App	851	151.5	3.8	277	7	US-10-245-882-213	Sequence 213, App
775	157.5	4.0	383	7	US-11-090-997-1040	Sequence 1040, App	852	151.5	3.8	277	7	US-10-245-882-213	Sequence 213, App
776	156.5	4.0	247	7	US-11-484-421-2	Sequence 2, Appl1	853	151.5	3.8	277	7	US-10-245-882-213	Sequence 213, App
777	156.5	4.0	394	6	US-10-527-571A-301	Sequence 301, App	854	151.5	3.8	277	7	US-10-245-882-213	Sequence 213, App
778	156	4.0	184	7	US-11-319-952-57	Sequence 57, Appl	855	151.5	3.8	277	7	US-10-245-882-213	Sequence 213, App
779	156	4.0	255	7	US-11-319-952-75	Sequence 75, Appl	856	151.5	3.8	277	7	US-10-245-882-213	Sequence 213, App
780	156	4.0	261	7	US-11-319-952-79	Sequence 79, Appl	857	151	3.8	247	7	US-11-415-342-6	Sequence 60, Appl1

854	151	3.8	703	6	US-10-529-348-316	Sequence 316, App	928	145.5	3.7	334	7	US-11-090-997-146	Sequence 146, App
856	150.5	3.8	685	6	US-10-567-630-33	Sequence 33, App1	929	145	3.7	372	7	US-10-669-920-208	Sequence 208, App
857	150.5	3.8	685	6	US-10-964-241-88	Sequence 88, App1	930	145	3.7	372	7	US-11-327-164-4	Sequence 4, App1
858	150.5	3.8	685	7	US-11-175-714-2	Sequence 2, App1	931	145	3.7	566	6	US-10-574-398-10	Sequence 10, App1
859	150.5	3.8	685	7	US-11-175-714-28	Sequence 28, App1	932	145	3.7	566	6	US-10-529-348-173	Sequence 173, App
860	150.5	3.8	685	7	US-11-175-714-34	Sequence 34, App1	933	145	3.7	566	6	US-11-066-316A-597	Sequence 597, App
861	150.5	3.8	685	7	US-11-175-714-36	Sequence 36, App1	934	145	3.7	581	7	US-11-066-316A-595	Sequence 595, App
862	150.5	3.8	685	7	US-11-175-714-38	Sequence 38, App1	935	144	3.7	234	7	US-11-476-636-14	Sequence 14, App1
864	150.5	3.8	685	7	US-11-178-724-20	Sequence 20, App1	936	144	3.7	244	7	US-11-247-886-10	Sequence 10, App1
865	150.5	3.8	685	7	US-11-644-243-2	Sequence 2, App1	937	144	3.7	683	7	US-11-371-354-55779	Sequence 55779, App
866	150.5	3.8	685	7	US-11-071-796A-19	Sequence 19, App1	938	143.5	3.6	246	6	US-10-538-002-124	Sequence 124, App
867	150.5	3.8	685	7	US-11-188-417A-20	Sequence 20, App1	939	143	3.6	119	7	US-11-486-448-100316	Sequence 100316, App
868	150.5	3.8	685	7	US-11-631-494-20	Sequence 20, App1	940	143	3.6	244	7	US-11-247-886-7	Sequence 7, App1
869	150	3.8	34	6	US-10-631-441-2439	Sequence 2439, App	941	142.5	3.6	428	7	US-11-345-903-14	Sequence 14, App1
870	150	3.8	113	7	US-11-507-474-22	Sequence 22, App1	942	142	3.6	611	7	US-11-302-782-3	Sequence 3, App1
871	150	3.8	267	6	US-10-524-434-589	Sequence 589, App	943	141.5	3.6	294	7	US-11-147-397-43	Sequence 43, App1
872	150	3.8	267	6	US-10-405-027-2920	Sequence 2920, App	944	141.5	3.6	372	6	US-10-533-519-906	Sequence 906, App
873	150	3.8	267	6	US-10-405-027-2922	Sequence 2922, App	945	141.5	3.6	373	6	US-10-669-920-217	Sequence 217, App
874	150	3.8	267	6	US-10-405-027-4107	Sequence 4107, App	946	141.5	3.6	373	6	US-10-796-307-808	Sequence 808, App
875	150	3.8	267	6	US-10-570-186-4	Sequence 4, App1	947	141.5	3.6	375	6	US-10-669-920-219	Sequence 219, App
876	150	3.8	276	6	US-10-544-944-16	Sequence 16, App1	948	141.5	3.6	375	6	US-10-796-307-806	Sequence 806, App
877	150	3.8	276	6	US-10-546-435-8	Sequence 8, App1	949	141.5	3.6	385	6	US-10-669-920-213	Sequence 213, App
878	150	3.8	276	6	US-10-529-348-840	Sequence 840, App	950	141.5	3.6	385	6	US-10-669-920-215	Sequence 215, App
879	150	3.8	276	6	US-11-292-215-1	Sequence 1, App1	951	141.5	3.6	385	6	US-10-796-307-805	Sequence 805, App
880	150	3.8	276	6	US-11-319-952-88	Sequence 88, App1	952	141.5	3.6	385	6	US-10-796-307-809	Sequence 809, App
881	150	3.8	276	7	US-11-043-842-177	Sequence 177, App	953	141	3.6	244	7	US-11-247-886-9	Sequence 9, App1
882	150	3.8	276	7	US-11-571-354-73049	Sequence 73049, App	954	141	3.6	246	6	US-10-533-520-2430	Sequence 2430, App
883	150	3.8	276	7	US-11-545-891-52	Sequence 52, App1	955	141	3.6	246	6	US-11-371-354-13796	Sequence 13796, App
884	150	3.8	703	7	US-11-066-316A-598	Sequence 598, App	956	141	3.6	246	7	US-11-371-354-65041	Sequence 65041, App
885	150	3.8	770	6	US-10-219-051B-156	Sequence 156, App	957	141	3.6	246	7	US-11-371-354-78522	Sequence 78522, App
886	150	3.8	770	6	US-10-219-051B-160	Sequence 160, App	958	141	3.6	246	7	US-11-478-199-942	Sequence 942, App
887	150	3.8	770	6	US-10-219-051B-160	Sequence 160, App	959	141	3.6	246	7	US-11-545-891-48	Sequence 48, App1
888	150	3.8	770	6	US-10-219-051B-160	Sequence 160, App	960	140.5	3.6	656	6	US-10-219-051B-14301	Sequence 14301, App
889	149.5	3.8	533	7	US-11-371-354-64691	Sequence 12196, A	961	140	3.5	148	6	US-10-652-846-2	Sequence 14301, A
890	149	3.8	644	6	US-11-066-316A-599	Sequence 599, App	962	140	3.5	148	6	US-11-295-040-2	Sequence 2, App1
891	149	3.8	644	6	US-10-777-288A-2134	Sequence 2134, App	963	140	3.5	971	6	US-10-760-320A-3217	Sequence 3217, App
892	149	3.8	770	6	US-10-219-051B-158	Sequence 158, App	964	140	3.5	4890	6	US-10-505-928-569	Sequence 569, App
893	149	3.8	770	6	US-10-219-051B-158	Sequence 158, App	965	139.5	3.5	207	7	US-11-357-337-4	Sequence 4, App1
894	149	3.8	770	6	US-10-219-051B-158	Sequence 158, App	966	139.5	3.5	1804	6	US-10-760-320A-3258	Sequence 3258, App
895	149	3.8	770	6	US-10-219-051B-158	Sequence 158, App	967	139.5	3.5	1804	6	US-10-669-920-1139	Sequence 1139, App
896	148.5	3.8	202	6	US-10-219-051B-12198	Sequence 12198, A	968	139.5	3.5	2000	6	US-10-533-520-1992	Sequence 1992, App
897	148.5	3.8	472	7	US-10-276-817B-14446	Sequence 14446, A	969	139	3.5	464	6	US-10-505-928-757	Sequence 757, App
898	148.5	3.8	1063	7	US-11-217-997-26	Sequence 26, App1	970	139	3.5	464	6	US-10-533-519-969	Sequence 969, App
899	148.5	3.8	1403	7	US-11-214-063A-1296	Sequence 1296, App	971	139	3.5	464	6	US-10-405-027-3522	Sequence 3522, App
900	148.5	3.8	1403	7	US-11-217-997-12	Sequence 12, App1	972	139	3.5	464	6	US-11-371-354-13350	Sequence 13350, A
901	148.5	3.8	1547	7	US-11-217-997-22	Sequence 22, App1	973	139	3.5	464	7	US-11-371-354-59423	Sequence 59423, A
902	148.5	3.8	1577	7	US-11-217-997-16	Sequence 16, App1	974	139	3.5	3888	7	US-11-526-137-115	Sequence 115, App
903	148.5	3.8	1577	7	US-11-217-997-20	Sequence 20, App1	975	139	3.5	3888	7	US-11-400-825-22	Sequence 22, App1
904	148.5	3.8	1620	7	US-11-217-997-42	Sequence 42, App1	976	138.5	3.5	158	7	US-10-511-937-2422	Sequence 2422, App1
905	148.5	3.8	1653	7	US-11-217-997-40	Sequence 40, App1	977	138.5	3.5	247	6	US-10-219-051B-8830	Sequence 8830, App
906	148.5	3.8	1786	6	US-10-796-280-770	Sequence 770, App	978	138.5	3.5	247	6	US-10-796-280-1136	Sequence 1136, App
907	148.5	3.8	4393	6	US-10-525-573-366	Sequence 366, App	979	138.5	3.5	247	6	US-10-796-280-1137	Sequence 1137, App
908	148.5	3.8	4393	6	US-11-450-360-1	Sequence 1, App1	980	138.5	3.5	247	6	US-11-484-421-222	Sequence 22, App1
909	148	3.8	113	7	US-11-507-474-23	Sequence 23, App1	981	138.5	3.5	247	7	US-11-362-260A-348	Sequence 348, App
910	148	3.8	367	6	US-10-527-571A-361	Sequence 361, App	982	138	3.5	226	7	US-11-292-215-11	Sequence 11, App1
911	148	3.8	464	6	US-10-743-643-2292	Sequence 2292, App	983	138	3.5	291	7	US-10-154-678-106	Sequence 106, App
912	147.5	3.7	683	7	US-11-066-316A-596	Sequence 596, App	984	138	3.5	345	6	US-11-412-329-106	Sequence 106, App
913	147.5	3.7	228	7	US-11-478-193-523	Sequence 523, App	985	138	3.5	345	7	US-10-777-288A-2019	Sequence 2019, App
914	147.5	3.7	4346	7	US-11-526-137-114	Sequence 114, App	986	137	3.5	892	6	US-10-669-920-1153	Sequence 1153, App
915	147.5	3.7	4347	7	US-11-526-137-116	Sequence 116, App	987	137	3.5	372	6	US-10-767-471-1010	Sequence 767, App
916	147.5	3.7	4391	7	US-11-183-325-56	Sequence 56, App1	988	137	3.5	1117	6	US-10-669-920-1142	Sequence 1142, App
917	147.5	3.7	4391	7	US-11-183-325-56	Sequence 56, App1	989	137	3.5	1117	6	US-10-669-920-1142	Sequence 1142, App
918	147	3.7	244	7	US-11-592-451-70	Sequence 70, App1	990	137	3.5	1506	6	US-10-796-307-559	Sequence 590, App
919	147	3.7	244	7	US-11-592-451-70	Sequence 70, App1	991	137	3.5	1506	6	US-10-796-307-559	Sequence 590, App
920	147	3.7	1029	6	US-11-247-886-6	Sequence 4, App1	992	137	3.5	2000	6	US-11-293-697-2765	Sequence 2765, App
921	146.5	3.7	277	6	US-10-669-920-1317	Sequence 1317, App	993	136.5	3.5	439	7	US-11-001-793-9105	Sequence 9105, App
922	146.5	3.7	277	6	US-10-245-882-214	Sequence 214, App	994	136.5	3.5	439	7	US-11-001-793-9105	Sequence 9105, App
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924	146	3.7	207	6	US-11-400-825-23	Sequence 23, App1	996	136.5	3.5	439	7	US-11-001-793-9105	Sequence 9105, App
925	146	3.7	207	6	US-10-405-027-3476	Sequence 3476, App	997	136.5	3.5	618	6	US-10-567-630-31	Sequence 31, App1
926	146	3.7	244	7	US-10-405-027-4911	Sequence 4911, App	998	136.5	3.5	618	6	US-10-245-882-301	Sequence 301, App1
927	146	3.7	622	7	US-11-247-886-5	Sequence 5, App1	999	136.5	3.5	618	7	US-11-178-724-19	Sequence 19, App1
					US-11-362-260A-347	Sequence 347, App	1000	136.5	3.5	618	7	US-11-071-796A-18	Sequence 18, App1

1001	136.5	3.5	618	7	US-11-188-417A-19	Sequence 19, Appl	1075	131.5	3.3	810	6	US-10-219-051B-8576	Sequence 8576, Ap
1002	136.5	3.5	618	7	US-11-231-494-19	Sequence 19, Appl	1076	131.5	3.3	810	6	US-10-219-051B-8580	Sequence 8580, Ap
1003	136.5	3.5	1198	7	US-11-217-997-14	Sequence 14, Appl	1077	131.5	3.3	810	6	US-10-245-882-3541	Sequence 361, App
1004	136	3.4	335	6	US-10-796-280-950	Sequence 950, App	1078	131.5	3.3	838	6	US-10-777-288A-3063	Sequence 3083, App
1005	136	3.4	345	6	US-10-796-280-952	Sequence 952, App	1079	131.5	3.3	1334	6	US-10-219-051B-276	Sequence 276, App
1006	136	3.4	345	6	US-11-371-354-60253	Sequence 60253, A	1080	131	3.3	76	7	US-11-254-183-46	Sequence 46, Appl
1007	136	3.4	352	6	US-10-405-027-4739	Sequence 4739, App	1081	131	3.3	76	7	US-11-253-865-46	Sequence 46, Appl
1009	136	3.4	525	6	US-10-964-241-114	Sequence 114, App	1082	131	3.3	328	7	US-11-371-354-63081	Sequence 63081, A
1010	136	3.4	666	6	US-10-449-902-41608	Sequence 41608, A	1083	131	3.3	1511	6	US-10-376-817B-15026	Sequence 15026, A
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1013	135.5	3.4	636	7	US-11-265-762-120	Sequence 100, App	1086	130.5	3.3	265	7	US-11-345-903-10	Sequence 10, Appl
1014	135.5	3.4	636	7	US-11-265-762-124	Sequence 124, App	1087	130.5	3.3	320	7	US-11-166-372-1796	Sequence 1796, Ap
1015	135	3.4	324	6	US-10-669-920-906	Sequence 906, App	1088	130.5	3.3	1233	6	US-10-777-288A-2595	Sequence 2595, Ap
1016	135	3.4	326	7	US-11-339-192-22	Sequence 22, Appl	1089	130.5	3.3	1398	7	US-10-777-288A-2595	Sequence 2595, Ap
1017	135	3.4	469	6	US-10-664-356-1770	Sequence 1770, Ap	1090	130.5	3.3	1450	7	US-11-217-997-4	Sequence 4, Appl
1018	135	3.4	469	7	US-11-246-999-41	Sequence 41, Appl	1091	130.5	3.3	1594	7	US-11-217-997-6	Sequence 6, Appl
1019	135	3.4	469	7	US-11-366-486-984	Sequence 984, App	1092	130	3.3	144	7	US-11-001-793-8901	Sequence 18, Appl
1020	135	3.4	469	7	US-11-001-793-9379	Sequence 9379, Ap	1093	130	3.3	300	7	US-11-001-793-9098	Sequence 9098, Ap
1021	135	3.4	494	6	US-10-664-356-1381	Sequence 1381, Ap	1095	130	3.3	490	6	US-10-970-823-132	Sequence 132, App
1022	135	3.4	494	6	US-10-796-280-1214	Sequence 1214, Ap	1096	130	3.3	490	6	US-10-964-241-310	Sequence 310, App
1023	135	3.4	494	6	US-10-796-280-1215	Sequence 1215, Ap	1097	129.5	3.3	254	7	US-11-427-112-10	Sequence 10, Appl
1024	135	3.4	494	6	US-10-796-280-1216	Sequence 1216, Ap	1098	129.5	3.3	271	7	US-11-427-112-11	Sequence 11, Appl
1025	135	3.4	494	7	US-11-366-486-765	Sequence 30, Appl	1099	129.5	3.3	381	6	US-10-533-519-401	Sequence 401, App
1026	135	3.4	494	7	US-11-366-486-765	Sequence 765, App	1100	129.5	3.3	381	7	US-11-371-354-68837	Sequence 68837, A
1027	135	3.4	494	7	US-11-001-793-6117	Sequence 6117, Ap	1101	129.5	3.3	534	6	US-10-376-817B-10189	Sequence 10189, A
1028	135	3.4	557	7	US-11-339-192-23	Sequence 23, Appl	1102	129.5	3.3	652	6	US-10-527-191-4	Sequence 4, Appl
1029	135	3.4	557	7	US-11-246-999-50	Sequence 50, Appl	1103	129.5	3.3	652	6	US-10-527-191-7	Sequence 7, Appl
1030	135	3.4	868	6	US-10-760-320A-3374	Sequence 3374, Ap	1104	129.5	3.3	652	6	US-10-527-191-39	Sequence 39, Appl
1031	134.5	3.4	260	6	US-10-530-643-14	Sequence 14, Appl	1105	129.5	3.3	652	6	US-10-527-191-42	Sequence 42, Appl
1032	134.5	3.4	332	6	US-10-540-845-3	Sequence 3, Appl	1106	129.5	3.3	652	6	US-10-533-519-622	Sequence 622, App
1033	134.5	3.4	352	6	US-10-540-845-2	Sequence 2, Appl	1107	129	3.3	191	6	US-10-703-032-118738	Sequence 118738
1034	134.5	3.4	358	6	US-10-540-845-4	Sequence 4, Appl	1108	128	3.3	244	7	US-11-247-886-8	Sequence 8, Appl
1035	134.5	3.4	1329	6	US-10-529-348-2237	Sequence 2237, Ap	1109	129	3.3	490	7	US-11-293-376-3621	Sequence 3621, Ap
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1037	134.5	3.4	1529	7	US-11-499-833-67	Sequence 67, Appl	1111	128.5	3.3	833	7	US-11-090-997-496	Sequence 496, App
1038	134	3.4	535	6	US-10-553-436-355	Sequence 355, Appl	1112	128.5	3.3	2923	6	US-10-570-909-35	Sequence 35, Appl
1039	134	3.4	587	7	US-11-030-653-32	Sequence 32, Appl	1113	128.5	3.3	2923	6	US-10-570-909-39	Sequence 39, Appl
1040	134	3.4	1786	6	US-10-519-328-2	Sequence 2, Appl	1114	128.5	3.3	2923	6	US-10-519-051B-210	Sequence 210, Appl
1041	134	3.4	1821	6	US-10-505-928-451	Sequence 451, App	1115	128.5	3.3	2923	6	US-10-219-051B-214	Sequence 214, App
1042	133.5	3.4	1821	6	US-10-519-328-1	Sequence 1, Appl	1116	128.5	3.3	2923	6	US-10-743-643-1049	Sequence 1049, App
1043	133.5	3.4	381	6	US-10-219-051B-795	Sequence 795, App	1117	128.5	3.3	2923	7	US-11-214-063A-932	Sequence 932, App
1044	133.5	3.4	381	6	US-10-219-051B-799	Sequence 799, App	1118	128	3.2	342	7	US-11-038-785-1	Sequence 1, Appl
1045	133	3.4	368	6	US-10-760-320A-3121	Sequence 3121, Ap	1119	128	3.2	357	6	US-10-540-845-9	Sequence 9, Appl
1046	133	3.4	810	6	US-10-544-553-4	Sequence 4, Appl	1120	128	3.2	353	6	US-10-540-845-17	Sequence 17, Appl
1047	133	3.4	810	6	US-10-219-051B-8574	Sequence 8574, Ap	1121	128	3.2	377	6	US-10-540-845-8	Sequence 8, Appl
1048	133	3.4	810	6	US-10-219-051B-8578	Sequence 8578, Ap	1122	128	3.2	383	6	US-10-540-845-10	Sequence 10, Appl
1049	133	3.4	1356	7	US-11-214-063A-1338	Sequence 1338, Ap	1123	128	3.2	383	6	US-10-540-845-16	Sequence 16, Appl
1050	132.5	3.4	310	6	US-10-570-909-7	Sequence 7, Appl	1124	128	3.2	383	7	US-11-166-372-2006	Sequence 2006, Ap
1051	132.5	3.4	310	7	US-11-090-997-1042	Sequence 1042, Ap	1125	128	3.2	383	7	US-11-001-793-7591	Sequence 7591, Ap
1052	132.5	3.4	682	6	US-10-777-288A-3971	Sequence 3971, Ap	1126	128	3.2	389	6	US-10-540-845-18	Sequence 18, Appl
1053	132.5	3.4	2136	7	US-11-218-141-1357	Sequence 1357, Ap	1127	128	3.2	689	6	US-10-669-920-1339	Sequence 1329, Ap
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1055	132.5	3.4	2725	5	US-11-066-316A-918	Sequence 918, App	1129	128	3.2	872	6	US-10-760-320A-4791	Sequence 4791, Ap
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1059	132	3.3	159	7	US-11-349-541-172	Sequence 172, App	1133	127	3.2	1609	6	US-10-533-519-115	Sequence 115, App
1060	132	3.3	159	7	US-11-344-932-172	Sequence 172, App	1134	127	3.2	2107	6	US-10-796-280-1108	Sequence 1108, Ap
1061	132	3.3	166	7	US-11-344-932-838	Sequence 838, App	1135	127	3.2	2107	6	US-10-796-307-671	Sequence 671, App
1062	132	3.3	236	7	US-11-371-354-56873	Sequence 56873, A	1136	127	3.2	2480	6	US-10-796-280-1106	Sequence 1106, Ap
1063	132	3.3	290	7	US-11-371-354-42160	Sequence 42160, A	1137	127	3.2	2480	6	US-10-796-307-669	Sequence 669, App
1064	132	3.3	290	7	US-11-371-354-73365	Sequence 73365, A	1138	127	3.2	3084	6	US-10-562-469-6	Sequence 6, Appl
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1067	132	3.3	443	6	US-10-760-320A-3401	Sequence 3401, Ap	1141	127	3.2	3116	6	US-10-796-307-670	Sequence 670, App
1068	132	3.3	1421	6	US-10-767-471-1009	Sequence 1209, App	1142	127	3.2	3122	6	US-10-219-051B-7721	Sequence 7721, App
1069	132	3.3	1421	6	US-10-767-471-1011	Sequence 1009, Ap	1143	126.5	3.2	448	6	US-10-219-051B-5598	Sequence 5198, Ap
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1071	132	3.3	1557	6	US-10-767-471-1011	Sequence 1011, Ap	1145	126.5	3.2	567	7	US-11-371-354-59045	Sequence 59045, A
1072	132	3.3	1587	6	US-10-767-471-1013	Sequence 1013, Ap	1146	126.5	3.2	844	6	US-10-777-288A-3415	Sequence 3415, Ap
1073	131.5	3.3	810	6	US-10-781-841-34	Sequence 34, Appl	1147	126.5	3.2	1050	7	US-11-265-762-114	Sequence 114, App
1074	131.5	3.3	810	6	US-10-544-553-2	Sequence 2, Appl	1148	126.5	3.2	1475	6	US-10-540-898-182	Sequence 182, App

1149	126	3.2	195	6	US-10-631-441-3019	Sequence 3019, Ap	1224	121	3.1	3396	6	US-10-219-051B-14303	Sequence 14303, A
1150	126	3.2	330	7	US-10-505-928-521	Sequence 521, App	1225	120.5	3.1	1431	7	US-11-352-664-2	Sequence 2, App11
1151	126	3.2	376	7	US-11-090-997-604	Sequence 604, App	1226	120.5	3.1	1801	6	US-10-219-051B-6292	Sequence 6292, Ap
1152	126	3.2	576	7	US-11-218-141-3820	Sequence 3820, Ap	1227	120	3.0	161	6	US-10-529-163-9	Sequence 9, App1
1153	126	3.2	576	7	US-11-218-141-3821	Sequence 3821, Ap	1228	120	3.0	161	7	US-11-066-316A-638	Sequence 638, App
1154	126	3.2	600	7	US-11-371-354-56941	Sequence 56941, A	1229	120	3.0	321	6	US-10-540-845-5	Sequence 5, App1
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1156	126	3.2	708	7	US-11-293-697-4328	Sequence 4329, Ap	1231	120	3.0	493	6	US-10-219-051B-2307	Sequence 2307, Ap
1157	126	3.2	999	5	US-09-976-858-189	Sequence 189, App	1232	120	3.0	493	6	US-10-219-051B-2311	Sequence 2311, Ap
1158	126	3.2	999	7	US-11-212-799-189	Sequence 189, App	1233	120	3.0	493	6	US-10-219-051B-2315	Sequence 2315, Ap
1159	126	3.2	1025	7	US-11-343-771-44	Sequence 44, App1	1234	120	3.0	493	6	US-11-267-942-3	Sequence 3, App1
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1161	125.5	3.2	554	7	US-11-166-372-2500	Sequence 2500, Ap	1236	120	3.0	747	7	US-11-240-891-58	Sequence 58, App1
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1163	125.5	3.2	728	7	US-11-450-056-2	Sequence 2, App11	1238	119.5	3.0	315	6	US-10-540-845-6	Sequence 6, App11
1164	125.5	3.2	775	6	US-10-990-328-10859	Sequence 10859, A	1239	119.5	3.0	864	7	US-11-090-997-1584	Sequence 1584, App
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1166	125	3.2	146	6	US-10-652-846-3	Sequence 3, App11	1241	119	3.0	164	7	US-11-449-541-178	Sequence 178, App
1167	125	3.2	146	7	US-11-295-040-3	Sequence 3, App11	1242	119	3.0	870	7	US-11-090-997-1582	Sequence 1582, Ap
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1170	124.5	3.2	531	6	US-10-990-328-10443	Sequence 10443, A	1245	118.5	3.0	375	7	US-11-289-102-304	Sequence 304, App
1171	124	3.1	531	6	US-10-760-320A-3418	Sequence 3418, Ap	1246	118.5	3.0	601	7	US-11-441-587-20	Sequence 20, App1
1172	124	3.1	559	6	US-10-219-051B-2026	Sequence 2026, Ap	1247	118.5	3.0	648	6	US-10-669-920-807	Sequence 807, App
1173	124	3.1	559	6	US-10-219-051B-2030	Sequence 2030, Ap	1248	118.5	3.0	728	6	US-10-570-046-3	Sequence 3, App11
1174	124	3.1	559	6	US-10-219-051B-3228	Sequence 3228, Ap	1249	118.5	3.0	728	6	US-10-527-195-1	Sequence 1, App11
1175	124	3.1	883	7	US-11-036-255A-8	Sequence 8512, Ap	1250	118.5	3.0	728	6	US-10-219-051B-13942	Sequence 13942, A
1176	124	3.1	883	7	US-11-036-255A-3	Sequence 3, App11	1251	118.5	3.0	728	6	US-10-555-925-1	Sequence 1, App11
1177	124	3.1	911	7	US-11-036-255A-6	Sequence 6, App11	1252	118.5	3.0	593	6	US-11-371-354-63803	Sequence 68503, A
1178	124	3.1	911	6	US-10-219-051B-8514	Sequence 8514, Ap	1253	118	3.0	728	7	US-11-178-424-1	Sequence 267, App
1179	124	3.1	911	7	US-11-226-554-89	Sequence 89, App1	1254	118	3.0	883	7	US-11-499-835-72	Sequence 72, App1
1180	124	3.1	911	7	US-11-248-718-89	Sequence 89, App1	1255	117.5	3.0	310	7	US-11-332-404-1	Sequence 1, App11
1181	124	3.1	911	7	US-11-248-718-89	Sequence 89, App1	1256	117.5	3.0	310	7	US-11-331-494-1	Sequence 1, App11
1182	124	3.1	911	7	US-11-371-354-55327	Sequence 55327, A	1257	117.5	3.0	332	7	US-11-231-494-46	Sequence 46, App1
1183	124	3.1	911	7	US-11-538-552-89	Sequence 89, App1	1258	117.5	3.0	332	7	US-11-188-417A-1	Sequence 1, App11
1184	123.5	3.1	239	7	US-11-043-842-178	Sequence 178, App	1259	117.5	3.0	332	7	US-11-188-417B-103	Sequence 103, App
1185	123.5	3.1	603	7	US-10-276-817B-8348	Sequence 8348, Ap	1260	117.5	3.0	332	7	US-11-331-494-60	Sequence 60, App1
1186	123.5	3.1	1533	6	US-10-533-365-236	Sequence 236, App	1261	117.5	3.0	955	7	US-11-166-372-2652	Sequence 2652, App
1188	123.5	3.1	1533	6	US-10-405-027-4060	Sequence 4060, Ap	1262	117.5	3.0	2000	6	US-10-533-519-732	Sequence 732, App
1190	123	3.1	330	6	US-10-669-920-211	Sequence 211, App	1263	117.5	3.0	2000	6	US-10-533-520-1101	Sequence 1101, App
1191	123	3.1	330	6	US-10-796-307-807	Sequence 807, App	1264	117.5	3.0	2214	6	US-10-570-909-25	Sequence 25, App1
1192	123	3.1	359	7	US-11-231-494-51	Sequence 51, App1	1265	117.5	3.0	2214	6	US-10-533-520-5266	Sequence 52, App1
1193	123	3.1	816	6	US-10-584-553-14	Sequence 14, App1	1266	117.5	3.0	2214	6	US-10-533-520-6253	Sequence 6253, Ap
1194	123	3.1	1573	6	US-10-786-280-1353	Sequence 1353, Ap	1267	117.5	3.0	2214	6	US-10-533-520-1728	Sequence 1728, Ap
1195	123	3.1	1573	6	US-10-524-434-588	Sequence 588, App	1268	117.5	3.0	2279	6	US-10-533-519-1278	Sequence 1278, Ap
1196	123	3.1	330	7	US-11-371-354-54991	Sequence 54991, A	1269	117.5	3.0	2279	6	US-11-253-869-47	Sequence 47, App1
1197	122.5	3.1	447	6	US-10-405-027-5488	Sequence 5488, Ap	1270	117	3.0	76	7	US-10-529-163-8	Sequence 8, App1
1198	122.5	3.1	650	6	US-10-219-051B-14611	Sequence 14611, A	1271	117	3.0	171	6	US-11-066-316A-639	Sequence 639, App
1199	122	3.1	650	6	US-10-533-519-1232	Sequence 1232, Ap	1272	117	3.0	858	7	US-11-090-997-434	Sequence 434, App
1200	122	3.1	676	6	US-10-219-051B-7994	Sequence 7994, Ap	1273	117	3.0	315	6	US-10-558-279-15	Sequence 15, App1
1201	122	3.1	676	6	US-10-219-051B-11815	Sequence 11815, A	1274	116.5	3.0	329	6	US-10-558-279-17	Sequence 17, App1
1202	122	3.1	879	6	US-10-276-817B-8349	Sequence 8349, Ap	1275	116.5	3.0	329	6	US-10-558-279-24	Sequence 24, App1
1203	122	3.1	3313	6	US-10-219-051B-208	Sequence 208, App	1276	116.5	3.0	329	6	US-10-558-279-24	Sequence 24, App1
1204	121.5	3.1	3313	6	US-10-219-051B-212	Sequence 212, App	1277	116.5	3.0	329	6	US-10-558-279-24	Sequence 24, App1
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